

1
SEQUENCE LISTING

<110> Trustees of Dartmouth College et al.

<120> NOVEL MOLECULES OF THE MULTI-DRUG AND TOXIN
EFFLUX (MATE) PROTEIN FAMILY AND USES THEREOF

<130> DCI-111PC

<150> 60/280, 621

<151> 2001-03-30

<160> 20

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 5738

<212> DNA

<213> Arabidopsis thaliana

<400> 1

```

ttttacata tttttgattc cattttcata agaaaatctt cagtatatta ttacattcat 60
atattattact tctttattat ttaaagtgat cattccaatt ttatatatag aaaattatct 120
atattatttat ggcaagggttg caacatataa aaaaaaagtt ggtatacaaa caaatatcta 180
aaataatccc ctctaaactc tcctagatac tcactcatca ctactcatct caagttcacg 240
tgactactta tataagcggtt gactacataa aggtaagata ttctctccac atatctcata 300
agttctatga tttttcttag tattgcatat atgttctcta tcctactagg atatatcaac 360
acaacataca caagttctca attgaattag aagctcatga gtaactataa ctgtatatat 420
agtttaactag attacgagta agaatgcaat tgtaaagcct ttaattgaa cttcttcttc 480
tttttttgat aaaagggtttt taattaaaaa aacaagtaat taaccattac aagctaggac 540
aactaagtca tacatggtga gagtagtgag agagttaagc aaaagcttaa tctagtcctt 600
ttaaagctca acaaacatag tagagattat aagatgtttg gtgtaaataa caacaatacc 660
cagtttgtag atgtgttttag aaaatagttt ggattatggg ctaaaatata taaattataa 720
gaaagatgat gtctaacgat tcaacatagc aaaagatgat gtacacaaat gtttttggtt 780
taccatgta aaaaaacaga acattagttg ttaagtttat aggtttatct tctacattaa 840
ttttcacaaac ttttttagtac cagaacgcac aatcaattaa gttttcatct tctatatata 900
ctgatctaaa aatattaata taaggtttgg gataattcaa tttaatcaca tcgtttataa 960
aaagcgggta actctacgat aactaaataa attgtgttat atgaaaaggg gaagtggcaa 1020
tgtagggaat ggaattgacg ttgatggcctt gaaaaagatg gccttatctt gcggaacaaa 1080
caattacata cagcacacgc actatataca actcacctgt gttggtctct gttgccatct 1140
tttatgttat tgttttccga ctgtcgctt cctttaacta atattataat tttaaagatg 1200
ttcataaatc acagtagaaa gcttggtttt gctaaaatga acatgacacg gatcatataa 1260
aaaatatatt ttacactata gctatatacc gatttaatct taggtacttt gaatcgtgct 1320
aaaactaaac ggccttctca aaacctctcc tcttttctc cctccctcag aaacctctcc 1380
atcgacaaat aacggttatgc aattctctaa acaatgctcg acaagcatgt gtttttagta 1440
atgctacaaac ttatttctct tttcaacgtc ctaagaggca tcaaaaagat caaagatctt 1500
ggaaccgagg tcctatgcaa ggaatcatta taaagtacca tgttattttt ttaaataaca 1560
tcgttttctt aatataatctt ataaataccg ttatttttac cgaaatttca tatatatgtc 1620
agttttatac tttgtacgat aacgcaaaaa actttaatta tcgcaaaaat tgtaaacggt 1680
attttctgctg tttagttatt taccaaaaat aaaatgacga ttgcaactta tttagttaaa 1740
atacaaaaaa aaactaatat attaatggag cggacggaat ttttttccaa aatcccgatg 1800
tgtaaatatg agaacgtttc gaggataact tacaaattaa acattaataa aaatgataaa 1860
gtgtagttag gagctaaatt gtgatagtaa acatctatct ctaatattat taaatgaatt 1920
ataatactat ttaaatcata gtattaaatt tctttaatta aaaatataaa taatttcaat 1980
ttaattctat accaaattaa cccgaaaata ttttatctaa catacacaaa gacacataaa 2040
agttttgata actgcctaaa aaaataagct tttgaattat taattagttg ttattcaatg 2100
ataaaaatac attatttgtc aactagttaa ttccaattac gcaaaatgat tcactttttt 2160
agtggaaaat atcaaagaaa aatgagaagt ttatatgaaa ataaactctt tcccactatg 2220

```

atgaatacat	gtaagaaaac	tttcatgaaa	agaaaactta	tttactcaat	ataaaaaatag	2280
aagactcttt	atctttcacg	agtaaaagtt	cacgaaaacc	atatttttcc	attgattaaa	2340
gaaatcatag	aagttaaaa	aatcaacaag	ggcaagccaa	aaacttctag	tgtgggattt	2400
acttaataga	agtatatata	ttacgatggt	tatgcgtagc	tattttccct	caatgagaag	2460
agaaaattcca	taatattggt	gtcttaagtt	tggacggaaa	taaagagcag	caaaaaagtt	2520
agggaaggaa	acctttgttt	tcttcaataa	ttatagaaaa	taattttctt	tattgattta	2580
gatattaaat	aagcaaagat	atgcatgctc	attacgtgtc	tataaataaa	aacacgtttg	2640
ttacatagcat	ctactataaa	cgttcctttt	gcttccccga	ttcttcgaaa	cacttattga	2700
tatcttcaga	cacaacaaat	taattacaga	gacagttaca	gaggaaaaag	atctatgacg	2760
gaaactgggtg	atgatcttgc	tacgggtgaag	aagccaatcc	cattttctcgt	tatcttcaaa	2820
gatttaaggt	gtgtgtttat	gtattcatga	aatgggtgatg	aaatttttga	aagaagtgat	2880
gcataacatt	agttttattta	tgtaaaattg	cagacatgta	ttcagtaggg	acacaactgg	2940
gcgagagatt	ctaggcatcg	cgtttccagc	agctttggct	ttagctgctg	atccaatcga	3000
ttctctgatt	gataccgctt	ttgtcggggc	tttaggagcg	gttcagctag	cggcgggttg	3060
agttttccatt	gccatattca	atcaagcttc	tagaattacg	atattcccac	ttgtgagcct	3120
cacaacttca	tttgtggcag	aggaagacac	gatggagaag	atgaaagaag	aagcaaaca	3180
agccaatctt	gttcatgcag	aaactatact	tgttcaagat	tctttggaaa	agggcatttc	3240
ttcacctaca	agtaacgata	ccaaccagcc	acagcaacct	ccaggtaaat	tccgcatatc	3300
tcactcgaca	ttgataactt	ttattaaagt	ttcgattggt	tttttactgt	tggtttcttc	3360
tctcgatctc	ttttgtttca	atltgttgtt	tttttggttg	tattaaactt	agctccggat	3420
acaaagtcaa	atagcggaaa	caaatcgaat	aaaaaggaga	agaggacat	tagaacagca	3480
tcaacagcta	tgatcttggg	gttaatcctt	ggccttgtgc	aagctatttt	cttgattttc	3540
agttcaaagt	tgcttctagg	cgtcatggga	gtgaaaccag	taagttttca	gaaatataca	3600
tattttgttg	ggatctatag	cataaaatgt	tttgactaat	ttgagttgaa	tttgataac	3660
agaattcacc	aatgtttatca	ccagcacaca	agtacttgag	catacgagct	ttgggggctc	3720
ctgcattgct	tctatctctt	gctatgcgaag	gcactcttct	tggattcaag	gacacaaaaa	3780
ctcctctctt	tgccactggt	aattaagttg	ttaaacttaga	tcactctttaa	tgatcactct	3840
ccttacttct	tataatatatt	tgcccttaatg	cgtgaaacag	tcgtagcaga	tgttatcaac	3900
atagttctcg	accccatctt	catttttgtg	cttcgtctag	ggatcatcgg	tcgagccatt	3960
gcccatgtca	tttctcagta	agagaaatca	ctaaaaaaat	tccacacatg	caaaagtgat	4020
cattattgaa	caaaatcgct	aggcgcactc	ttgtttttct	acagctataa	atagacttgt	4080
gaagtcataa	cctcaaacaa	aaacaaatga	tttgtttgtg	tacgtgaagg	tacttcatga	4140
ctctaataat	gttcgtcttc	ctcgcaaaga	aagttaattt	gattccacca	aacttcgggg	4200
atttgcagtt	tggaaagttc	cttaaaaaatg	gtacgtatgg	atgcatattt	attaaaagtt	4260
gtggttcttg	caataatatt	ttttttttaa	aacaagatcc	gtcgtaggag	ctaattgcaca	4320
gagtcacaaa	ataaattaac	aaaaaattta	tctatataat	aatagaattc	aatcaaataa	4380
ggtctatatt	taaaatatatt	aatatatttga	aatatatagt	taagaaaatg	agaaatgtgg	4440
atatatgtct	aacaagtata	gtattaaaaa	tgaagggtct	actattgctg	gcgaggacca	4500
tagcagtgac	gttttgtcag	accttagcag	cagcaatggc	ggcgcggctg	ggtacaacac	4560
caatggctgc	ttttcagatt	tgtttacaag	tatggttaac	ttcttctctt	ctcaatgatg	4620
gtcttgccgt	tgctggtcag	gtaatcatgt	tttctcgttg	tattaattta	tgtatagttt	4680
atatggttga	tcaagttgta	tgtagaaaat	gatcattcaa	tacgttgacg	gcgattctgg	4740
cttgttcgtt	tgctgagaag	gactataaca	aagtgactgc	tgttgcatcc	cgtgttctac	4800
aggttcggtc	caaaaatcac	attaccaaac	ctttctttaa	aaataaaaata	atttgttaac	4860
taaaacagaa	atgaatttga	tacgcagatg	ggttttgtgt	taggacttgg	actgtccgtt	4920
tttgttgac	taggtctcta	ctttgggtgcc	ggagttttct	ccaaggaccc	tgctgttatt	4980
cacctcatgg	ccatcggaat	accggtaact	aataatcaaa	taataattac	tatagtataa	5040
aatcattttt	aaaagaattt	tactaatgag	aagagggttat	atatattttat	gcagtttata	5100
gcagcaacgc	agccaataaa	ctctctcgcc	tttgtatttg	atggagtcaa	ttttggagca	5160
tctgattttg	cttaccactgc	atactccatg	gtatgcacac	tatatatact	atgaaatgat	5220
taaaattcct	tttttttttt	ttgaaatgac	ttaaactttg	tctatctttt	tttcttgtaa	5280
tccaattatg	ataaatcagg	tgggagtgcc	ggccataagc	attgcagcag	taatatatat	5340
ggcaaagacc	aatggtttca	taggaatatg	gatagctctt	acaatctata	tggctctccg	5400
ggctattact	ggaattgcca	ggtattttaa	ttgggccttt	actatagccc	actatagtag	5460
aagcagtatt	tgactgagtg	tttgaattta	tgcaggatgg	cgacaggaac	tggaccgtgg	5520
aggttcttgc	gtggacgatc	atcctcttca	tcttcctagg	acttagttta	tttataacga	5580
gttgcattct	ttcttccttc	ttcgtttttg	tttatggttc	ttgtgtttgt	ttttcaacat	5640
tttgttcgag	agaccgttat	catattatca	gtttcacata	aataatgcat	atttttaagt	5700

cattaaaata tggagccctc tgcctcact ggcttttc

5738

<210> 2

<211> 1868

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (118)...(1695)

<400> 2

aaataatccc ctctaaactc tcctagatac tcactcatca ctactcatct caagttcacg 60
 tgactactta tataagcggt gactacataa agagacagtt acagaggaaa aagatct atg 120
 Met
 1

acg gaa act ggt gat gat ctt gct acg gtg aag aag cca atc cca ttt 168
 Thr Glu Thr Gly Asp Asp Leu Ala Thr Val Lys Lys Pro Ile Pro Phe
 5 10 15

ctc gtt atc ttc aaa gat tta aga cat gta ttc agt agg gac aca act 216
 Leu Val Ile Phe Lys Asp Leu Arg His Val Phe Ser Arg Asp Thr Thr
 20 25 30

ggg cga gag att cta ggc atc gcg ttt cca gca gct ttg gct tta gct 264
 Gly Arg Glu Ile Leu Gly Ile Ala Phe Pro Ala Ala Leu Ala Leu Ala
 35 40 45

gct gat cca atc gat tct ctg att gat acc gct ttt gtc ggg cgt tta 312
 Ala Asp Pro Ile Asp Ser Leu Ile Asp Thr Ala Phe Val Gly Arg Leu
 50 55 60 65

gga gcg gtt cag cta gcg gcg gtt gga gtt tcc att gcc ata ttc aat 360
 Gly Ala Val Gln Leu Ala Ala Val Gly Val Ser Ile Ala Ile Phe Asn
 70 75 80

caa gct tct aga att acg ata ttc cca ctt gtg agc ctc aca act tca 408
 Gln Ala Ser Arg Ile Thr Ile Phe Pro Leu Val Ser Leu Thr Thr Ser
 85 90 95

ttt gtg gca gag gaa gac acg atg gag aag atg aaa gaa gaa gca aac 456
 Phe Val Ala Glu Glu Asp Thr Met Glu Lys Met Lys Glu Glu Ala Asn
 100 105 110

aaa gcc aat ctt gtt cat gca gaa act ata ctt gtt caa gat tct ttg 504
 Lys Ala Asn Leu Val His Ala Glu Thr Ile Leu Val Gln Asp Ser Leu
 115 120 125

gaa aag ggc att tct tca cct aca agt aac gat acc aac cag cca cag 552
 Glu Lys Gly Ile Ser Ser Pro Thr Ser Asn Asp Thr Asn Gln Pro Gln
 130 135 140 145

caa cct cca gct ccg gat aca aag tca aat agc gga aac aaa tcg aat 600
 Gln Pro Pro Ala Pro Asp Thr Lys Ser Asn Ser Gly Asn Lys Ser Asn
 150 155 160

aaa aag gag aag agg acc att aga aca gca tca aca gct atg atc ttg	648
Lys Lys Glu Lys Arg Thr Ile Arg Thr Ala Ser Thr Ala Met Ile Leu	
165 170 175	
ggg tta atc ctt ggc ctt gtg caa gct att ttc ttg att ttc agt tca	696
Gly Leu Ile Leu Gly Leu Val Gln Ala Ile Phe Leu Ile Phe Ser Ser	
180 185 190	
aag ttg ctt cta ggc gtc atg gga gtg aaa cca aat tca cca atg tta	744
Lys Leu Leu Leu Gly Val Met Gly Val Lys Pro Asn Ser Pro Met Leu	
195 200 205	
tca cca gca cac aag tac ttg agc ata cga gct ttg ggg gct cct gca	792
Ser Pro Ala His Lys Tyr Leu Ser Ile Arg Ala Leu Gly Ala Pro Ala	
210 215 220 225	
ttg ctt cta tct ctt gct atg caa ggc atc ttt cgt gga ttc aag gac	840
Leu Leu Leu Ser Leu Ala Met Gln Gly Ile Phe Arg Gly Phe Lys Asp	
230 235 240	
acc aaa act cct ctc ttt gcc act gtc gta gca gat gtt atc aac ata	888
Thr Lys Thr Pro Leu Phe Ala Thr Val Val Ala Asp Val Ile Asn Ile	
245 250 255	
gtt ctc gac ccc atc ttc att ttt gtg ctt cgt cta ggg atc atc ggt	936
Val Leu Asp Pro Ile Phe Ile Phe Val Leu Arg Leu Gly Ile Ile Gly	
260 265 270	
gca gcc att gcc cat gtc att tct cag tac ttc atg act cta ata ttg	984
Ala Ala Ile Ala His Val Ile Ser Gln Tyr Phe Met Thr Leu Ile Leu	
275 280 285	
ttc gtc ttc ctc gca aag aaa gtt aat ttg att cca cca aac ttc ggg	1032
Phe Val Phe Leu Ala Lys Lys Val Asn Leu Ile Pro Pro Asn Phe Gly	
290 295 300 305	
gat ttg cag ttt gga agg ttc ctt aaa aat ggg cta cta ttg ctg gcg	1080
Asp Leu Gln Phe Gly Arg Phe Leu Lys Asn Gly Leu Leu Leu Leu Ala	
310 315 320	
agg acc ata gca gtg acg ttt tgt cag acc tta gca gca gca atg gcg	1128
Arg Thr Ile Ala Val Thr Phe Cys Gln Thr Leu Ala Ala Ala Met Ala	
325 330 335	
gcg cgg ctg ggt aca aca cca atg gct gct ttt cag att tgt tta caa	1176
Ala Arg Leu Gly Thr Thr Pro Met Ala Ala Phe Gln Ile Cys Leu Gln	
340 345 350	
gta tgg tta act tct tct ctt ctc aat gat ggt ctt gcc gtt gct ggt	1224
Val Trp Leu Thr Ser Ser Leu Leu Asn Asp Gly Leu Ala Val Ala Gly	
355 360 365	
cag gcg att ctg gct tgt tgc ttt gct gag aag gac tat aac aaa gtg	1272
Gln Ala Ile Leu Ala Cys Ser Phe Ala Glu Lys Asp Tyr Asn Lys Val	
370 375 380 385	

5

```

act gct gtt gca tcc cgt gtt cta cag atg ggt ttt gtg tta gga ctt 1320
Thr Ala Val Ala Ser Arg Val Leu Gln Met Gly Phe Val Leu Gly Leu
390 395 400

gga ctg tcc gtt ttt gtt gga cta ggt ctc tac ttt ggt gcc gga gtt 1368
Gly Leu Ser Val Phe Val Gly Leu Gly Leu Tyr Phe Gly Ala Gly Val
405 410 415

ttc tcc aag gac cct gct gtt att cac ctc atg gcc atc gga ata ccg 1416
Phe Ser Lys Asp Pro Ala Val Ile His Leu Met Ala Ile Gly Ile Pro
420 425 430

ttt ata gca gca acg cag cca ata aac tct ctc gcc ttt gta ttg gat 1464
Phe Ile Ala Ala Thr Gln Pro Ile Asn Ser Leu Ala Phe Val Leu Asp
435 440 445

gga gtc aat ttt gga gca tct gat ttt gct tac act gca tac tcc atg 1512
Gly Val Asn Phe Gly Ala Ser Asp Phe Ala Tyr Thr Ala Tyr Ser Met
450 455 460 465

gtg gga gtg gcg gcc ata agc att gca gca gta ata tat atg gca aag 1560
Val Gly Val Ala Ala Ile Ser Ile Ala Ala Val Ile Tyr Met Ala Lys
470 475 480

acc aat ggt ttc ata gga ata tgg ata gct ctt aca atc tat atg gct 1608
Thr Asn Gly Phe Ile Gly Ile Trp Ile Ala Leu Thr Ile Tyr Met Ala
485 490 495

ctc cgg gct att act gga att gcc agg atg gcg aca gga act gga ccg 1656
Leu Arg Ala Ile Thr Gly Ile Ala Arg Met Ala Thr Gly Thr Gly Pro
500 505 510

tgg agg ttc ttg cgt gga cga tca tcc tct tca tct tcc taggacttag 1705
Trp Arg Phe Leu Arg Gly Arg Ser Ser Ser Ser Ser Ser
515 520 525

tttattttata acgagtttgca tctcttcttc cttcttcggt tttgtttatg gttcttgtgt 1765
ttgttttttca acatttttggt cgagagaccg ttatcatatt atcagttttca cataaataat 1825
gcatattttt aagtcattaa aataaaaaaaaa aaaaaaaaaaa aaa 1868

```

<210> 3

<211> 526

<212> PRT

<213> Arabidopsis thaliana

<400> 3

```

Met Thr Glu Thr Gly Asp Asp Leu Ala Thr Val Lys Lys Pro Ile Pro
1 5 10 15
Phe Leu Val Ile Phe Lys Asp Leu Arg His Val Phe Ser Arg Asp Thr
20 25 30
Thr Gly Arg Glu Ile Leu Gly Ile Ala Phe Pro Ala Ala Leu Ala Leu
35 40 45
Ala Ala Asp Pro Ile Asp Ser Leu Ile Asp Thr Ala Phe Val Gly Arg
50 55 60
Leu Gly Ala Val Gln Leu Ala Ala Val Gly Val Ser Ile Ala Ile Phe
65 70 75 80
Asn Gln Ala Ser Arg Ile Thr Ile Phe Pro Leu Val Ser Leu Thr Thr
85 90 95

```

Ser	Phe	Val	Ala	Glu	Glu	Asp	Thr	Met	Glu	Lys	Met	Lys	Glu	Glu	Ala
			100					105					110		
Asn	Lys	Ala	Asn	Leu	Val	His	Ala	Glu	Thr	Ile	Leu	Val	Gln	Asp	Ser
		115					120					125			
Leu	Glu	Lys	Gly	Ile	Ser	Ser	Pro	Thr	Ser	Asn	Asp	Thr	Asn	Gln	Pro
		130					135				140				
Gln	Gln	Pro	Pro	Ala	Pro	Asp	Thr	Lys	Ser	Asn	Ser	Gly	Asn	Lys	Ser
					150					155					160
Asn	Lys	Lys	Glu	Lys	Arg	Thr	Ile	Arg	Thr	Ala	Ser	Thr	Ala	Met	Ile
				165					170					175	
Leu	Gly	Leu	Ile	Leu	Gly	Leu	Val	Gln	Ala	Ile	Phe	Leu	Ile	Phe	Ser
			180					185					190		

Ser	Lys	Leu	Leu	Gly	Val	Met	Gly	Val	Lys	Pro	Asn	Ser	Pro	Met	
		195				200					205				
Leu	Ser	Pro	Ala	His	Lys	Tyr	Leu	Ser	Ile	Arg	Ala	Leu	Gly	Ala	Pro
		210				215					220				
Ala	Leu	Leu	Leu	Ser	Leu	Ala	Met	Gln	Gly	Ile	Phe	Arg	Gly	Phe	Lys
225					230					235					240
Asp	Thr	Lys	Thr	Pro	Leu	Phe	Ala	Thr	Val	Val	Ala	Asp	Val	Ile	Asn
				245					250					255	
Ile	Val	Leu	Asp	Pro	Ile	Phe	Ile	Phe	Val	Leu	Arg	Leu	Gly	Ile	Ile
			260					265					270		
Gly	Ala	Ala	Ile	Ala	His	Val	Ile	Ser	Gln	Tyr	Phe	Met	Thr	Leu	Ile
		275					280					285			
Leu	Phe	Val	Phe	Leu	Ala	Lys	Lys	Val	Asn	Leu	Ile	Pro	Pro	Asn	Phe
		290				295					300				
Gly	Asp	Leu	Gln	Phe	Gly	Arg	Phe	Leu	Lys	Asn	Gly	Leu	Leu	Leu	Leu
305					310					315					320
Ala	Arg	Thr	Ile	Ala	Val	Thr	Phe	Cys	Gln	Thr	Leu	Ala	Ala	Ala	Met
				325					330					335	
Ala	Ala	Arg	Leu	Gly	Thr	Thr	Pro	Met	Ala	Ala	Phe	Gln	Ile	Cys	Leu
			340					345					350		
Gln	Val	Trp	Leu	Thr	Ser	Ser	Leu	Leu	Asn	Asp	Gly	Leu	Ala	Val	Ala
		355					360					365			
Gly	Gln	Ala	Ile	Leu	Ala	Cys	Ser	Phe	Ala	Glu	Lys	Asp	Tyr	Asn	Lys
		370				375					380				
Val	Thr	Ala	Val	Ala	Ser	Arg	Val	Leu	Gln	Met	Gly	Phe	Val	Leu	Gly
385					390					395					400
Leu	Gly	Leu	Ser	Val	Phe	Val	Gly	Leu	Gly	Leu	Tyr	Phe	Gly	Ala	Gly
				405					410					415	
Val	Phe	Ser	Lys	Asp	Pro	Ala	Val	Ile	His	Leu	Met	Ala	Ile	Gly	Ile
			420					425					430		
Pro	Phe	Ile	Ala	Ala	Thr	Gln	Pro	Ile	Asn	Ser	Leu	Ala	Phe	Val	Leu
		435					440					445			
Asp	Gly	Val	Asn	Phe	Gly	Ala	Ser	Asp	Phe	Ala	Tyr	Thr	Ala	Tyr	Ser
		450				455					460				
Met	Val	Gly	Val	Ala	Ala	Ile	Ser	Ile	Ala	Ala	Val	Ile	Tyr	Met	Ala
465					470					475					480
Lys	Thr	Asn	Gly	Phe	Ile	Gly	Ile	Trp	Ile	Ala	Leu	Thr	Ile	Tyr	Met
				485					490					495	
Ala	Leu	Arg	Ala	Ile	Thr	Gly	Ile	Ala	Arg	Met	Ala	Thr	Gly	Thr	Gly
			500					505					510		
Pro	Trp	Arg	Phe	Leu	Arg	Gly	Arg	Ser	Ser	Ser	Ser	Ser	Ser		
		515					520					525			

<211> 5737

<212> DNA

<213> *Arabidopsis thaliana*

<400> 4

```

tttctacata tttttgattc catttttcata agaaaatctt cagtatatta ttacattcat 60
attttattact tcttttattat tttaaagtgat cattccaatt ttatatatag aaaattatatt 120
attttatttat ggcaagggttg caacatataa aaaaaaagtt ggtatacaaaa caaatatcta 180
aaataatccc ctctaaactc tcctagatac tcactcatca ctactcatct caagttcacg 240
tgactactta tataagcggtt gactacataa aggttaagata ttctctccac atatctcata 300
agttctatga tttttcttag tattgcatat atgttctcta tcctactagg atatatcaac 360
acaacataca caagttctca attgaattag aagctcatga gtaactataa ctgtatatat 420
agttaactag attacgagta agaatgcaat tgtaaagcct tttaattgaa cttcttcttc 480
tttttttgat aaaaggtttt taattaaanaa aacaagtaat taaccattac aagctaggac 540
aactaagtca tacatggtga gagtagtgag agagttaagc aaaagcttaa tctagtcctt 600
ttaaaagcta acaaacatag tagagattat aagatgtttg gtgtaaataa caacaatacc 660
cagtttgtag atgtgttttag aaaatagttt ggattatggg ctaaaatata taaattataa 720
gaaagatgat gtctaacgat tcaacatagc aaaagatgat gtacacaaaat gtttttggtt 780
taccatgta aaaaaacaga acattagttg ttaagtttat aggtttatatt tctacattaa 840
ttttcacaac ttttttagtac cagaacgcac aatcaattaa gttttcatct tctatatata 900
ctgatctaaa aatattaata taaggtttgg gataattcaa tttaatcaca tcggtttataa 960
aaagcggtta actctacgat aactaaataa attgtgttat atgaaaaggg gaagtggaac 1020
tgtaggtaat ggaattgacg ttgatggcct gaaaaagatg gccttatctt gcggaacaaa 1080
caattacata cagcacacgc actatataca actcacctgt gttgggtctt gttgccatct 1140
tttatgttat tgttttccga ctgtcgcctt cctttaacta atattataat tttaaagatg 1200
ttcataaatc acagtagaaa gcttggtttt gctaaaatga acatgacacg gatcatacaa 1260
aaaatatatt ttacactata gctatatacc gatttaatct taggtacttt gaatcggtgt 1320
aaaactaaac ggcccttctca aaaccctccc tcttttcttc cctccctcag aaaccctccc 1380
atcgacaaat aacggttatgc aattctctaa acaatgctcg acaagcatgt gtttttagta 1440
atgctacaac ttatttctct tttcaacgtc ctaagaggca tcaaaaagat caaagatctt 1500
ggaaaccgagg tcctatgcaa ggaatcatta taaagtacca tgttattttt ttaaataaca 1560
tcggtttctt aatataaatt ataaataaccg ttattttttac cgaaatttca tatatatgtc 1620
agttttatac tttgtacgat aacgccaaaa actttaatta tcgccaaaat tgtaaacggt 1680
attttcgtcg tttagttatt taccaaaaaat aaaatgacga ttgcaactta tttagttaaa 1740
atacaaaaaa aaactaatat attaattgag cggacggaat ttttttccaa aatcccgatg 1800
tgtaaatatg agaacgtttc gaggataact tacaatttaa acattataaa aaatgataaa 1860
gtgtagttag gagctaaatt gtgatagtaa acatctatct ctaatatatt taaatgaatt 1920
ataatactat tttaatcata gtattaaatt tctttaatta aaaatataaa taatttcaat 1980
ttaattctat accaaattaa cccgaaaata ttttatctaa catacacaaa gacacataaa 2040
agttttgata actgcctaaa aaaataagct tttgaattat taattagttg ttattcaatg 2100
ataaaataac attatttggt aactagttaa ttccaattac gcaaaatgat tcaacttttt 2160
agtggaaaaa atcaaagaaa aatgagaagt ttatatgaaa ataaactctt tcccactatg 2220
atgaatacat gtaagaaaac tttcatgaaa agaaaactta tttactcaat ataaaaatag 2280
aagactcttt atctttcacg agtaaaaagt cacgaaaacc atattttcct attgattaaa 2340
gaaatcatag aagttaaaat aatcaacaag ggcaagccaa aaacttctag tgtgggattt 2400
acttaataga agtatatata ttacgatgtt tatgctgacc tattttccct caatgagaag 2460
agaaattcca taatattggt gtcttaagtt tggacggaaa taaagagcag caaaaaagtt 2520
agggaaggaa acctttgttt tcttcaataa ttatagaaaa taatttcttt tattgattta 2580
gatattaaat aagcaaagat atgcatgctc attacgtgtc tataaataaa aacacgtttg 2640
tacatagcat ctactataaa cgttcctttt gcttccccga ttcttcgaaa cacttattga 2700
tatcttcaga cacaacaaat taattacaga gacagttaca gaggaaaaag atctatgacg 2760
gaaactggtg atgatcttgc tacggtgaag aagccaatcc catttctcgt tatcttcaaa 2820
gatttaaggt gtgtgtttat gtattcatga aatggtgatg aaatttttga aagaagtgat 2880
gcataacatt agtttattta tgtaaaattg cagacatgta ttcagtaggg acacaactgg 2940
gcgagagatt ctaggcacatg cgtttccagc agctttggct ttagctgctg atccaatcgc 3000
ttctctgatt gataccgctt ttgtcgggag tttaggagcg gttcagctag cggcgggttg 3060
agtttccatt gccatattca atcaagcttc tagaattacg atattccac ttgtgagcct 3120
cacaacttca tttgtggcag aggaagacac tagtgagaag atgaaagaag aagcaacaaa 3180
agccaactct gttcatgcag aaactatact tgttcaagat tctttggaaa agggcatttc 3240
ttcacctaca agtaacgata ccaaccagcc acagcaacct ccaggtaaat tccgcatatc 3300

```

```

tcaactcgaca ttgataaactt ttattaaagt ttcgattgtt tttttactgt tgggtttcttc 3360
tctcgatctc ttttggtttca atttgttggt tttttggttg tattaaactt agctccggat 3420
acaaagtcaa atagcggaaa caaatcgaat aaaaaggaga agaggacat tagaacagca 3480
tcaacagcta tgatcttggg gttaatcctt ggccttgtgc aagctathtt cttgattttc 3540
agttcaaagt tgcttctagg cgtcatggga gtgaaaccag taagttttca gaaatataca 3600
tattttgttg ggatctatag cataaaatgt tttgactaat ttgagttgaa tttggataac 3660
agaattcacc aatgttatca ccagcacaca agtacttgag catacgagct ttgggggctc 3720
ctgcattgct tctatctctt gctatgcaag gcatctttcg tggattcaag gacacaaaaa 3780
ctcctctctt tgccactggt aattaagttg ttaacttaga tcatctttaa tgatcactct 3840
ccttacttct tataatatatt tgccttaatg cgtgaaacag tcgtagcaga tgttatcaac 3900
atagttctcg accccatctt catttttctg cttcgtctag ggatcatcgg tgcagccatt 3960
gcccatgtca tttctcagta agagaaatca ctaaaaaaat tccacacatg caaaagtgat 4020
cattattgaa caaaatcgct aggcgcactc ttgtttttct acagctataa atagacttgt 4080
gaagtcataa cctcaaacaa aaacaaatga tttgtttgtg tacgtgaagg tacttcatga 4140
ctctaataatt gttcgtcttc ctgcgaaaga aagttaattt gattccacca aacttcgggg 4200
atttgcagtt tggaaggttc cttaaaaatg gtacgtatgg atgcataatt attaaaagtt 4260
gtggttcttg caataatatt tttttttaaa aacaagatcc gtcgtaggag ctaatgcaca 4320
gagtcacaaa ataaattaac aaaaaattta tctatataat aatagaattc aatcaaataa 4380
ggtctatatt taaaatatgg aatattttga aatatatagt taagaaaatg agaaatgtgg 4440
atatatgtct aacaagtata gtattaaaaa tgaaagggct actattgctg gcgaggacca 4500
tagcagtgac gttttgtcag accttagcag cagcaatggc ggcgcggtg ggtacaacac 4560
caatggctgt tttcagattt gtttacaagt atggtttaact tcttctcttc tcaatgatgg 4620
tcttgccgtt gctggtcagg taatcatgtt ttctcgttgt attaatttat gtatagttta 4680
tatggttgat caagttgtat gtagaaaatg atcattcaat acgttgacag cgattctggc 4740
ttgttcgttt gctgagaagg actataacaa agtgactgct gttgcatccc gtgttctaca 4800
ggttcggtcc aaaaatcaca ttaccaaacc tttctttaaa aataaaaataa ttgtgtaact 4860
aaaacagaaa tgaatttgat acgcagatgg gttttgtgtt aggacttggg ctgtccgttt 4920
ttgttggaact aggtctctac tttggtgccc gagttttctc caaggaccct gctgttattc 4980
acctcatggc catcggaata ccggttaacta ataatacaat aataattact atagtataaa 5040
aatcatttta aaagaatttt actaatgaga agagggttata tatatttatg cagtttatag 5100
cagcaacgca gccataaaac tctctcgcc tttgtattgga tggagtcaat tttggagcat 5160
ctgattttgc ttacactgca tactccatgg tatgcacact atatatacta tgaaatgatt 5220
aaaattcctt tttttttttt tgaaatgact taaactttgt ctatcttttt ttcttgtaat 5280
ccaattatga taaatcaggt gggagtggcg gccataagca ttgcagcagt aatatatatg 5340
gcaaagacca atggtttcat aggaatatgg atagctctta caatctatat ggctctccgg 5400
gctattactg gaattgccag gtattttaa tgggccttta ctatagccca ctatagtaga 5460
agcagtattt gactgagtggt ttgaatttat gcaggatggc gacaggaact ggaccgtgga 5520
ggttcttgcg tggacgatca tctcttctcat cttcctagga cttagtttat ttataacgag 5580
ttgcatctct tcttctctct tcgtttttgt ttatggttct tgtgtttgtt tttcaacatt 5640
ttgttcgaga gaccgttatc atattatcag tttcacataa ataatgcata tttttaagtc 5700
attaaaaatat ggagccctct gccctcactg gcttttc 5737

```

<210> 5

<211> 1867

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (118)...(1182)

<400> 5

```

aaataatccc ctctaaactc tcctagatac tcaactcatca ctactcatct caagttcacg 60
tgactactta tataagcggt gactacataa agagacaggt acagaggaaa aagatct atg 120

```

Met

1

acg gaa act ggt gat gat ctt gct acg gtg aag aag cca atc cca ttt	168
Thr Glu Thr Gly Asp Asp Leu Ala Thr Val Lys Lys Pro Ile Pro Phe	
5 10 15	
ctc gtt atc ttc aaa gat tta aga cat gta ttc agt agg gac aca act	216
Leu Val Ile Phe Lys Asp Leu Arg His Val Phe Ser Arg Asp Thr Thr	
20 25 30	
ggg cga gag att cta ggc atc gcg ttt cca gca gct ttg gct tta gct	264
Gly Arg Glu Ile Leu Gly Ile Ala Phe Pro Ala Ala Leu Ala Leu Ala	
35 40 45	
gct gat cca atc gct tct ctg att gat acc gct ttt gtc ggg cgt tta	312
Ala Asp Pro Ile Ala Ser Leu Ile Asp Thr Ala Phe Val Gly Arg Leu	
50 55 60 65	
gga gcg gtt cag cta gcg gcg gtt gga gtt tcc att gcc ata ttc aat	360
Gly Ala Val Gln Leu Ala Ala Val Gly Val Ser Ile Ala Ile Phe Asn	
70 75 80	
caa gct tct aga att acg ata ttc cca ctt gtg agc ctc aca act tca	408
Gln Ala Ser Arg Ile Thr Ile Phe Pro Leu Val Ser Leu Thr Thr Ser	
85 90 95	
ttt gtg gca gag gaa gac acg atg gag aag atg aaa gaa gaa gca aac	456
Phe Val Ala Glu Glu Asp Thr Met Glu Lys Met Lys Glu Glu Ala Asn	
100 105 110	
aaa gcc aat ctt gtt cat gca gaa act ata ctt gtt caa gat tct ttg	504
Lys Ala Asn Leu Val His Ala Glu Thr Ile Leu Val Gln Asp Ser Leu	
115 120 125	
gaa aag ggc att tct tca cct aca agt aac gat acc aac cag cca cag	552
Glu Lys Gly Ile Ser Ser Pro Thr Ser Asn Asp Thr Asn Gln Pro Gln	
130 135 140 145	
caa cct cca gct ccg gat aca aag tca aat agc gga aac aaa tcg aat	600
Gln Pro Pro Ala Pro Asp Thr Lys Ser Asn Ser Gly Asn Lys Ser Asn	
150 155 160	
aaa aag gag aag agg acc att aga aca gca tca aca gct atg atc ttg	648
Lys Lys Glu Lys Arg Thr Ile Arg Thr Ala Ser Thr Ala Met Ile Leu	
165 170 175	
ggg tta atc ctt ggc ctt gtg caa gct att ttc ttg att ttc agt tca	696
Gly Leu Ile Leu Gly Leu Val Gln Ala Ile Phe Leu Ile Phe Ser Ser	
180 185 190	
aag ttg ctt cta ggc gtc atg gga gtg aaa cca aat tca cca atg tta	744
Lys Leu Leu Leu Gly Val Met Gly Val Lys Pro Asn Ser Pro Met Leu	
195 200 205	
tca cca gca cac aag tac ttg agc ata cga gct ttg ggg gct cct gca	792
Ser Pro Ala His Lys Tyr Leu Ser Ile Arg Ala Leu Gly Ala Pro Ala	
210 215 220 225	

10

```

ttg ctt cta tct ctt gct atg caa ggc atc ttt cgt gga ttc aag gac 840
Leu Leu Leu Ser Leu Ala Met Gln Gly Ile Phe Arg Gly Phe Lys Asp
230 235 240

acc aaa act cct ctc ttt gcc act gtc gta gca gat gtt atc aac ata 888
Thr Lys Thr Pro Leu Phe Ala Thr Val Val Ala Asp Val Ile Asn Ile
245 250 255

gtt ctc gac ccc atc ttc att ttt gtg ctt cgt cta ggg atc atc ggt 936
Val Leu Asp Pro Ile Phe Ile Phe Val Leu Arg Leu Gly Ile Ile Gly
260 265 270

gca gcc att gcc cat gtc att tct cag tac ttc atg act cta ata ttg 984
Ala Ala Ile Ala His Val Ile Ser Gln Tyr Phe Met Thr Leu Ile Leu
275 280 285

ttc gtc ttc ctc gca aag aaa gtt aat ttg att cca cca aac ttc ggg 1032
Phe Val Phe Leu Ala Lys Lys Val Asn Leu Ile Pro Pro Asn Phe Gly
290 295 300 305

gat ttg cag ttt gga agg ttc ctt aaa aat ggg cta cta ttg ctg gcg 1080
Asp Leu Gln Phe Gly Arg Phe Leu Lys Asn Gly Leu Leu Leu Leu Ala
310 315 320

agg acc ata gca gtg acg ttt tgt cag acc tta gca gca gca atg gcg 1128
Arg Thr Ile Ala Val Thr Phe Cys Gln Thr Leu Ala Ala Ala Met Ala
325 330 335

gcg cgg ctg ggt aca aca cca atg gct gtt ttc aga ttt gtt tac aag 1176
Ala Arg Leu Gly Thr Thr Pro Met Ala Val Phe Arg Phe Val Tyr Lys
340 345 350

tat ggt taacttcttc tcttctcaat gatggtcttg ccgttgctgg tcaggcgatt 1232
Tyr Gly
355

ctggcttggt cgtttgctga gaaggactat aacaaagtga ctgctgttgc atcccggtgt 1292
ctacagatgg gttttgtgtt aggacttgga ctgtccgttt ttgttggtact aggtctctac 1352
tttggtgccg gagttttctc caaggaccct gctgttattc acctcatggc catcggaata 1412
ccgtttatag cagcaacgca gccataaac tctctcgctt ttgtattgga tggagtcaat 1472
tttgagcat ctgattttgc ttacactgca tactccatgg tgggagtggc ggccataagc 1532
attgcagcag taatatatat ggcaaagacc aatggtttca taggaatatg gatagctctt 1592
acaatctata tggctctccg ggctattact ggaattgcca ggatggcgac aggaactgga 1652
ccgtggaggt tcttgctggg acgatcatcc tcttcatctt cctaggactt agtttattta 1712
taacgagttg catctcttct tccttcttctg tttttgttta tggttcttgt gtttggtttt 1772
caacattttg ttcgagagac cgttatcata ttatcagttt cacataaata atgcatattt 1832
ttaagtcatt aaaataaaaa aaaaaaaaaa aaaaa 1867

```

<210> 6

<211> 355

<212> PRT

<213> Arabidopsis thaliana

<400> 6

```

Met Thr Glu Thr Gly Asp Asp Leu Ala Thr Val Lys Lys Pro Ile Pro
1 5 10 15

```

Phe Leu Val Ile Phe Lys Asp Leu Arg His Val Phe Ser Arg Asp Thr
 20 25 30
 Thr Gly Arg Glu Ile Leu Gly Ile Ala Phe Pro Ala Ala Leu Ala Leu
 35 40 45
 Ala Ala Asp Pro Ile Ala Ser Leu Ile Asp Thr Ala Phe Val Gly Arg
 50 55 60
 Leu Gly Ala Val Gln Leu Ala Ala Val Gly Val Ser Ile Ala Ile Phe
 65 70 75 80
 Asn Gln Ala Ser Arg Ile Thr Ile Phe Pro Leu Val Ser Leu Thr Thr
 85 90 95
 Ser Phe Val Ala Glu Glu Asp Thr Met Glu Lys Met Lys Glu Glu Ala
 100 105 110
 Asn Lys Ala Asn Leu Val His Ala Glu Thr Ile Leu Val Gln Asp Ser
 115 120 125
 Leu Glu Lys Gly Ile Ser Ser Pro Thr Ser Asn Asp Thr Asn Gln Pro
 130 135 140
 Gln Gln Pro Pro Ala Pro Asp Thr Lys Ser Asn Ser Gly Asn Lys Ser
 145 150 155 160
 Asn Lys Lys Glu Lys Arg Thr Ile Arg Thr Ala Ser Thr Ala Met Ile
 165 170 175
 Leu Gly Leu Ile Leu Gly Leu Val Gln Ala Ile Phe Leu Ile Phe Ser
 180 185 190
 Ser Lys Leu Leu Leu Gly Val Met Gly Val Lys Pro Asn Ser Pro Met
 195 200 205
 Leu Ser Pro Ala His Lys Tyr Leu Ser Ile Arg Ala Leu Gly Ala Pro
 210 215 220
 Ala Leu Leu Leu Ser Leu Ala Met Gln Gly Ile Phe Arg Gly Phe Lys
 225 230 235 240
 Asp Thr Lys Thr Pro Leu Phe Ala Thr Val Val Ala Asp Val Ile Asn
 245 250 255
 Ile Val Leu Asp Pro Ile Phe Ile Phe Val Leu Arg Leu Gly Ile Ile
 260 265 270
 Gly Ala Ala Ile Ala His Val Ile Ser Gln Tyr Phe Met Thr Leu Ile
 275 280 285
 Leu Phe Val Phe Leu Ala Lys Lys Val Asn Leu Ile Pro Pro Asn Phe
 290 295 300
 Gly Asp Leu Gln Phe Gly Arg Phe Leu Lys Asn Gly Leu Leu Leu Leu
 305 310 315 320
 Ala Arg Thr Ile Ala Val Thr Phe Cys Gln Thr Leu Ala Ala Ala Met
 325 330 335
 Ala Ala Arg Leu Gly Thr Thr Pro Met Ala Val Phe Arg Phe Val Tyr
 340 345 350
 Lys Tyr Gly
 355

<210> 7

<211> 5738

<212> DNA

<213> Arabidopsis thaliana

<400> 7

```

tttctacata tttttgattc cattttcata agaaaatctt cagtatatta ttacattcat 60
atttattact tctttattat ttaaagtgat cattccaatt ttatatatag aaaattatTT 120
atttatTTat ggcaaggTtg caacatataa aaaaaaagtt ggtatacaaa caaatatcta 180
aaataatccc ctctaaactc tcctagatac tcactcatca ctactcatct caagttcacg 240
tgactactta tataagcgTt gactacataa aggtaagata ttctctccac atatctcata 300
agttctatga tttttcttag tattgcatat atgttctcta tcctactagg atatatcaac 360
acaacataca caagttctca attgaattag aagctcatga gtaactataa ctgtatatat 420

```

agttaactag	attacgagta	agaatgcaat	tgtaaagcct	tttaattgaa	cttcttcttc	480
tttttttgat	aaaaggtttt	taattaaana	aacaagtaat	taaccattac	aagctaggac	540
aactaagtca	tacatgttga	gagtagtgag	agagttaagc	aaaagcttaa	tctagtcctt	600
ttaaaagcta	acaaacatag	tagagattat	aagatgtttg	gtgtaaataa	caacaatacc	660
cagtttgtac	atgtgtttag	aaaatagttt	ggattatggg	ctaaaaatata	taaattataa	720
gaaagatgat	gtctaacgat	tcaacatagc	aaaagatgat	gtacacaaat	gtttttgttt	780
taccatgta	aaaaaacaga	acattagttg	ttaagtttat	aggtttattt	tctacattaa	840
ttttcacaa	tttttagtac	cagaacgcac	aatcaattaa	gttttcatct	tctatatata	900
ctgatctaaa	aatattaata	taagggttgg	gataattcaa	tttaatcaca	tcgtttataa	960
aaagcggtta	actctacgat	aactaaataa	attgtgttat	atgaaaaggg	gaagtggcaa	1020
tgtaggtaat	ggaattgacg	ttgatggcct	gaaaaagatg	gccttatctt	gcggaacaaa	1080
caattacata	cacgacacgc	actatataca	actcacctgt	gttggtctct	gttgccatct	1140
tttatgttat	tgttttccga	ctgtcgccct	cctttaacta	atattataat	tttaaagatg	1200
ttcataaata	acagtagaaa	gcttggtttt	gctaaaatga	acatgacacg	gatcatacaa	1260
aaaatatatt	ttacactata	gctatatacc	gatttaactt	taggtacttt	gaatcgtgct	1320
aaaactaaac	ggccttctca	aaacctccc	tctttctctc	cctccctcag	aaacctctcc	1380
atcgacaaat	aacggttatgc	aattctctaa	acaatgctcg	acaagcatgt	gttttttagta	1440
atgctacaac	ttatttctct	tttcaacgtc	ctaagaggca	tcaaaaagat	caaagatctt	1500
ggaaccgagg	tcctatgcaa	ggaatcatta	taaagtacca	tgttattttt	ttaaataaca	1560
tcgttttctt	aatataattt	ataaataccg	ttattttttac	cgaaatttca	tatatatgtc	1620
agttttatac	tttgtagcat	aacgccaaaa	actttaatta	tcgccaaaat	tgtaaaccgt	1680
attttcgtcg	tttagttatt	taccaaaaat	aaaatgacga	ttgcaactta	tttagttaa	1740
atacaaaaaa	aaactaatat	attaattgag	cggacggaat	ttttttccaa	aatcccgatg	1800
tgtaaatatg	agaacgtttc	gaggataact	tacaaattaa	acattaataa	aatgataaaa	1860
gtgtagttag	gagctaaatt	gtgatagtaa	acatctatct	ctaataattt	taaatgaatt	1920
ataatactat	tttaatacata	gtattaaatt	tctttaatta	aaaatatata	taatttcaat	1980
ttaattctat	accaaattaa	cccgaaaata	ttttatctaa	catacacaaa	gacacataaa	2040
agttttgata	actgcctaaa	aaaataagct	tttgaattat	taattagttg	ttattcaatg	2100
ataaaataac	attattttgtc	aactagtga	ttccaattac	gcaaaatgat	tcactttttt	2160
agtggaaaat	atcaaagaaa	aatgagaagt	ttatatgaaa	ataaactctt	tcccactatg	2220
atgaatacat	gtaagaaaa	tttcatgaaa	agaaaactta	tttactcaat	ataaaaaatag	2280
aagactcttt	atcttttcacg	agtaaaagt	cacgaaaacc	atattttctt	attgattaaa	2340
gaaatcatag	aagttaaaa	aatcaacaag	ggcaagccaa	aaacttctag	tgtgggattt	2400
acttaataga	agtatatata	ttacgatgtt	tatgcgtacc	tattttccct	caatgagaag	2460
agaaattcca	taatatgtgt	gtotaaagt	tggaacgaaa	taaagagcag	caaaaaagtt	2520
agggaaggaa	acctttgttt	tcttcaataa	ttatagaaaa	taatttcttt	tattgattta	2580
gatattaaat	aagcaaagat	atgcatgctc	attacgtgtc	tataaataaa	aacacgtttg	2640
tacatagcat	ctactataaa	cgttcccttt	gcttccccga	ttcttcgaaa	cacttattga	2700
tatcttcaga	cacaacaaat	taattacaga	gacagttaca	gaggaaaaag	atctatgacg	2760
gaaactggtg	atgatcttgc	tacgggtgaag	aagccaatcc	catttctcgt	tatcttcaaa	2820
gatttaagg	gtgtgtttat	gtattcatga	aatgggtgat	aaatttttga	aagaagtgat	2880
gcataacatt	agttttatta	tgtaaaattg	cagacatgta	ttcagtaggg	acacaactgg	2940
gcgagagatt	ctaggcatcg	cgtttccagc	agctttgggt	ttagctgctg	atccaatcgc	3000
ttctctgatt	gataccgctt	ttgtcgggcg	tttaggagcg	gttcagctag	cggcggttgg	3060
agtttccatt	gccatattca	atcaagcttc	tagaattacg	atattccac	ttgtgagcct	3120
cacaacttca	tttgtggcag	aggaagacac	gatggagaag	atgaaagaag	aagcaaaca	3180
agccaatctt	gttcatgcag	aaactatact	tgttcaagat	tctttggaaa	agggcatttc	3240
ttcacctaca	agtaacgata	ccaaccagcc	acagcaacct	ccaggtaaat	tccgcatatc	3300
tactctgaca	ttgataactt	ttattaaagt	ttcgattggt	tttttactgt	tggtttcttc	3360
tctcgatctc	ttttgtttca	atttgttgtt	tttttggttg	tattaaactt	agctccggat	3420
acaaagtcaa	atagcggaaa	caaatcgaat	aaaaaggaga	agaggacat	tagaagacga	3480
tcaacagcta	tgatcttggg	gttaatcctt	ggccttgtgc	aagctatttt	cttgattttc	3540
agttcaaagt	tgcttctagg	cgtcatggga	gtgaaaccag	taagttttca	gaaatataca	3600
tattttgttg	ggatctatag	cataaaatgt	tttgactaat	ttgagttgaa	tttgataaac	3660
agaattcacc	aatgttatca	ccagcacaca	agtacttgag	catacgagct	ttgggggctc	3720
ctgcattgct	tctatctctt	gctatgcaag	gcatctttcg	tggattcaag	gacacaaaa	3780
ctcctctctt	tgccactgat	aattaagttg	ttaacttaga	tcatctttaa	tgatcactct	3840
ccttacttct	tataatattt	tgccttaatg	cgtgaaacag	tcgtagcaga	tgttatcaac	3900
atagttctcg	accccatctt	catttttgtg	cttcgtctag	ggatcatcgg	tcgagccatt	3960

```

gccccatgtca tttctcagta agagaaatca ctaaaaaaat tccacacatg caaaagtgat 4020
cattattgaa caaaatcgct aggcgcactc ttgtttttct acagctataa atagacttgt 4080
gaagtcataa cctcaaacaa aaacaaatga tttgtttgtg tacgtgaagg tacttcatga 4140
ctctaataatt gttcgtcttc ctgcgaaaga aagttaattt gattccacca aacttcgggg 4200
atttgcagtt tggaagggtc cttaaaaatg gtacgtatgg atgcatattt attaaaagtt 4260
gtgggttcttg caataatatt tttttttaaa aacaagatcc gtcgtaggag ctaatgcaca 4320
gagtcacaaa ataaattaac aaaaaattta tctatataat aatagaattc aatcaataa 4380
ggtctatatt taaaatattg aatattttga aatatatagt taagaaaatg agaaatgtg 4440
atatatgtct aacaagtata gtattaaaaa tgaaagggct actattgctg gcgaggacca 4500
tagcagtgc gttttgtcag accttagcag cagcaatggc ggcgcggtg ggtacaacac 4560
caatggctgc ttttcagatt tgtttacaag tatggttaac ttcttctctt ctcaatgatg 4620
gtcttgccgt tgctggtcag gtaatcatgt tttctcgttg tattaattta tgtatagttt 4680
atatggttga tcaagttgta tgtagaaaat gatcattcaa tacgttgcatg gcgattctgg 4740
cttggttcgtt tgctgagaag gactataaca aagtgactgc tgttgcattc cgtgttctac 4800
aggttcggtc caaaaatcac attaccaaac ctttctttaa aaataaaaata attgtgtaac 4860
taaaacagaa atgaatttga tacgcagatg ggttttgtgt taggacttgg actgtccgtt 4920
tttgttgga ctaggtctcta ctttggtgcc ggagttttct ccaaggacct tgctgttatt 4980
cacctcatgg ccctcggaat accggttaact aataatcaaa taataattac tatagtataa 5040
aaatcatttt aaaagaattt tactaatgag aagagggtat atatatattt gcagtttata 5100
gcagcaacgc agccaataaa ctctctcgcc ttgtatttgg atggagtcaa ttttgagca 5160
tctgattttg cttacactgc atactccatg gtatgcacac tatatatact atgaaatgat 5220
taaaattcct tttttttttt ttgaaatgac ttaaaactttg tctatctttt tttcttgtaa 5280
tccaattatg ataaatcagg tgggagtggc ggccataagc attgcagcag taatatatat 5340
ggcaaagacc aatggtttca taggaatatg gatagctctt acaatctata tggctctccg 5400
ggctattact ggaattgcca ggtattttaa ttgggccttt actatagccc actatagtag 5460
aagcagtatt tgactgagtg tttgaattta tgcaggatgg cgacaggaac tggaccgtgg 5520
aggttcttgc gtggacgac atcctcttca tcttcttagg acttagttta tttataacga 5580
gttgcattct ttcttcttct ttcgtttttg tttatgggtc ttgtgtttgt ttttcaacat 5640
tttgttcgag agaccgttat catattatca gtttcacata aataatgcat atttttaagt 5700
cattaaaata tggagccctc tgccctcact ggcttttc 5738

```

<210> 8

<211> 1950

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> CDS

<222> (118)...(870)

<400> 8

```

aaataatccc ctctaaactc tcctagatac tcaactcatca ctactcatct caagttcacg 60
tgactactta tataagcggt gactacataa agagacagtt acagaggaaa aagatct atg 120
Met
1

```

```

acg gaa act ggt gat gat ctt gct acg gtg aag aag cca atc cca ttt 168
Thr Glu Thr Gly Asp Asp Leu Ala Thr Val Lys Lys Pro Ile Pro Phe
5 10 15

```

```

ctc gtt atc ttc aaa gat tta aga cat gta ttc agt agg gac aca act 216
Leu Val Ile Phe Lys Asp Leu Arg His Val Phe Ser Arg Asp Thr Thr
20 25 30

```

```

ggg cga gag att cta ggc atc gcg ttt cca gca gct ttg gct tta gct 264
Gly Arg Glu Ile Leu Gly Ile Ala Phe Pro Ala Ala Leu Ala Leu Ala
35 40 45

```

```

gct gat cca atc gct tct ctg att gat acc gct ttt gtc ggg cgt tta 312
Ala Asp Pro Ile Ala Ser Leu Ile Asp Thr Ala Phe Val Gly Arg Leu
50 55 60 65

gga gcg gtt cag cta gcg gcg gtt gga gtt tcc att gcc ata ttc aat 360
Gly Ala Val Gln Leu Ala Ala Val Gly Val Ser Ile Ala Ile Phe Asn
70 75 80

caa gct tct aga att acg ata ttc cca ctt gtg agc ctc aca act tca 408
Gln Ala Ser Arg Ile Thr Ile Phe Pro Leu Val Ser Leu Thr Thr Ser
85 90 95

ttt gtg gca gag gaa gac acg atg gag aag atg aaa gaa gaa gca aac 456
Phe Val Ala Glu Glu Asp Thr Met Glu Lys Met Lys Glu Glu Ala Asn
100 105 110

aaa gcc aat ctt gtt cat gca gaa act ata ctt gtt caa gat tct ttg 504
Lys Ala Asn Leu Val His Ala Glu Thr Ile Leu Val Gln Asp Ser Leu
115 120 125

gaa aag ggc att tct tca cct aca agt aac gat acc aac cag cca cag 552
Glu Lys Gly Ile Ser Ser Pro Thr Ser Asn Asp Thr Asn Gln Pro Gln
130 135 140 145

caa cct cca gct ccg gat aca aag tca aat agc gga aac aaa tcg aat 600
Gln Pro Pro Ala Pro Asp Thr Lys Ser Asn Ser Gly Asn Lys Ser Asn
150 155 160

aaa aag gag aag agg acc att aga aca gca tca aca gct atg atc ttg 648
Lys Lys Glu Lys Arg Thr Ile Arg Thr Ala Ser Thr Ala Met Ile Leu
165 170 175

ggg tta atc ctt ggc ctt gtg caa gct att ttc ttg att ttc agt tca 696
Gly Leu Ile Leu Gly Leu Val Gln Ala Ile Phe Leu Ile Phe Ser Ser
180 185 190

aag ttg ctt cta ggc gtc atg gga gtg aaa cca aat tca cca atg tta 744
Lys Leu Leu Leu Gly Val Met Gly Val Lys Pro Asn Ser Pro Met Leu
195 200 205

tca cca gca cac aag tac ttg agc ata cga gct ttg ggg gct cct gca 792
Ser Pro Ala His Lys Tyr Leu Ser Ile Arg Ala Leu Gly Ala Pro Ala
210 215 220 225

ttg ctt cta tct ctt gct atg caa ggc atc ttt cgt gga ttc aag gac 840
Leu Leu Leu Ser Leu Ala Met Gln Gly Ile Phe Arg Gly Phe Lys Asp
230 235 240

acc aaa act cct ctc ttt gcc act gat aat taagttggta acttagatca 890
Thr Lys Thr Pro Leu Phe Ala Thr Asp Asn
245 250

tctttaatga tcaactctcct tacttcttat aatattttgc cttaatgcgt gaaacagtcg 950
tagcagatgt tatcaacata gttctcgacc ccatcttcat ttttgtgctt cgtctaggga 1010
tcatcggtgc agccattgcc catgtcattt ctcaagtactt catgactcta atattgttcg 1070
tcttcctcgc aaagaaagtt aatttgattc caccaaactt cggggatttg cagtttgga 1130
ggttccttaa aaatgggcta ctattgctgg cgaggaccat agcagtgacg ttttgtcaga 1190
ccttagcagc agcaatggcg gcgcggctgg gtacaacacc aatggctgct tttcagattt 1250

```

15

```

gtttacaagt atgggttaact tcttctcttc tcaatgatgg tcttgccggt gctgggtcagg 1310
cgattctggc ttgttcgttt gctgagaagg actataacaa agtgactgct gttgcatccc 1370
gtgttctaca gatgggtttt gtgttaggac ttggactgtc cgtttttgtt ggactaggtc 1430
tctacttttg tgccggagtt ttctccaagg accctgctgt tattcacctc atggccatcg 1490
gaataccggt tatagcagca acgcagccaa taaactctct cgcctttgta ttggatggag 1550
tcaatttttg agcatctgat ttgtcttaca ctgcatactc catggtggga gtggcggcca 1610
taagcattgc agcagtaata tatatggcaa agaccaatgg ttcatagga atatggatag 1670
ctcttacaat ctatatggct ctccgggcta ttactggaat tgccaggatg gcgacaggaa 1730
ctggaccgtg gaggttcttg cgtggacgat catcctcttc atcttcctag gacttagttt 1790
atttataacg agttgcatct cttcttccct cttcgttttt gtttatgggt cttgtgtttg 1850
tttttcaaca ttttgttcga gagaccgtta tcatattatc agtttcacat aaataatgca 1910
tatttttaag tcattaaaat aaaaaaaaaa aaaaaaaaaa 1950

```

<210> 9

<211> 251

<212> PRT

<213> Arabidopsis thaliana

<400> 9

```

Met Thr Glu Thr Gly Asp Asp Leu Ala Thr Val Lys Lys Pro Ile Pro
 1          5          10          15
Phe Leu Val Ile Phe Lys Asp Leu Arg His Val Phe Ser Arg Asp Thr
 20          25          30
Thr Gly Arg Glu Ile Leu Gly Ile Ala Phe Pro Ala Ala Leu Ala Leu
 35          40          45
Ala Ala Asp Pro Ile Ala Ser Leu Ile Asp Thr Ala Phe Val Gly Arg
 50          55          60
Leu Gly Ala Val Gln Leu Ala Ala Val Gly Val Ser Ile Ala Ile Phe
 65          70          75          80
Asn Gln Ala Ser Arg Ile Thr Ile Phe Pro Leu Val Ser Leu Thr Thr
 85          90          95
Ser Phe Val Ala Glu Glu Asp Thr Met Glu Lys Met Lys Glu Glu Ala
100          105          110
Asn Lys Ala Asn Leu Val His Ala Glu Thr Ile Leu Val Gln Asp Ser
115          120          125
Leu Glu Lys Gly Ile Ser Ser Pro Thr Ser Asn Asp Thr Asn Gln Pro
130          135          140

Gln Gln Pro Pro Ala Pro Asp Thr Lys Ser Asn Ser Gly Asn Lys Ser
145          150          155          160
Asn Lys Lys Glu Lys Arg Thr Ile Arg Thr Ala Ser Thr Ala Met Ile
165          170          175
Leu Gly Leu Ile Leu Gly Leu Val Gln Ala Ile Phe Leu Ile Phe Ser
180          185          190
Ser Lys Leu Leu Leu Gly Val Met Gly Val Lys Pro Asn Ser Pro Met
195          200          205
Leu Ser Pro Ala His Lys Tyr Leu Ser Ile Arg Ala Leu Gly Ala Pro
210          215          220
Ala Leu Leu Leu Ser Leu Ala Met Gln Gly Ile Phe Arg Gly Phe Lys
225          230          235          240
Asp Thr Lys Thr Pro Leu Phe Ala Thr Asp Asn
245          250

```

<210> 10

<211> 523

<212> PRT

<213> Arabidopsis thaliana

<400> 10

```

Met Thr Glu Thr Gly Asp Asp Leu Ala Thr Val Lys Lys Pro Ile Pro
 1      5      10      15
Phe Leu Val Ile Phe Lys Asp Leu Arg His Val Phe Ser Arg Asp Thr
      20      25      30
Thr Gly Arg Glu Ile Leu Gly Ile Ala Phe Pro Ala Ala Leu Ala Leu
      35      40      45
Ala Ala Asp Pro Ile Ala Ser Leu Ile Asp Thr Ala Phe Val Gly Arg
      50      55      60
Leu Gly Ala Val Gln Leu Ala Ala Val Gly Val Ser Ile Ala Ile Phe
65      70      75      80
Asn Gln Ala Ser Arg Ile Thr Ile Phe Pro Leu Val Ser Leu Thr Thr
      85      90      95
Ser Phe Val Ala Glu Glu Asp Thr Met Glu Lys Met Lys Glu Glu Ala
      100      105      110
Asn Lys Ala Asn Leu Val His Ala Glu Thr Ile Leu Val Gln Asp Ser
      115      120      125
Leu Glu Lys Gly Ile Ser Ser Pro Thr Ser Asn Asp Thr Asn Gln Pro
      130      135      140
Gln Gln Pro Pro Ala Pro Asp Thr Lys Ser Asn Ser Gly Asn Lys Ser
145      150      155      160
Asn Lys Lys Glu Lys Arg Thr Ile Arg Thr Ala Ser Thr Ala Met Ile
      165      170      175
Leu Gly Leu Ile Leu Gly Leu Val Gln Ala Ile Phe Leu Ile Phe Ser
      180      185      190
Ser Lys Leu Leu Leu Gly Val Met Gly Val Lys Pro Asn Ser Pro Met
      195      200      205
Leu Ser Pro Ala His Lys Tyr Leu Ser Ile Arg Ala Leu Gly Ala Pro
      210      215      220
Ala Leu Leu Leu Ser Leu Ala Met Gln Gly Ile Phe Arg Gly Phe Lys
225      230      235      240
Asp Thr Lys Thr Pro Leu Phe Ala Thr Val Val Ala Asp Val Ile Asn
      245      250      255
Ile Val Leu Asp Pro Ile Phe Ile Phe Val Leu Arg Leu Gly Ile Ile
      260      265      270
Gly Ala Ala Ile Ala His Val Ile Ser Gln Tyr Phe Met Thr Leu Ile
      275      280      285
Leu Phe Val Phe Leu Ala Lys Lys Val Asn Leu Ile Pro Pro Asn Phe
      290      295      300

Gly Asp Leu Gln Phe Gly Arg Phe Leu Lys Asn Gly Leu Leu Leu Leu
305      310      315      320
Ala Arg Thr Ile Ala Val Thr Phe Cys Gln Thr Leu Ala Ala Ala Met
      325      330      335
Ala Ala Arg Leu Gly Thr Thr Pro Met Ala Ala Phe Gln Ile Cys Leu
      340      345      350
Gln Val Trp Leu Thr Ser Ser Leu Leu Asn Asp Gly Leu Ala Val Ala
      355      360      365
Gly Gln Ala Leu Ala Cys Ser Phe Ala Glu Lys Asp Tyr Asn Lys Val
      370      375      380
Thr Ala Val Ala Ser Arg Val Leu Gln Met Gly Phe Val Leu Gly Leu
385      390      395      400
Gly Leu Ser Val Phe Val Gly Leu Gly Leu Tyr Phe Gly Ala Gly Val
      405      410      415
Phe Ser Lys Asp Pro Ala Val Ile His Leu Met Ala Ile Gly Ile Pro
      420      425      430
Phe Ala Ala Thr Gln Pro Ile Asn Ser Leu Ala Phe Val Leu Asp Gly
      435      440      445

```


17

```

Val Asn Phe Gly Ala Ser Asp Phe Ala Tyr Thr Ala Tyr Ser Met Val
  450                               455           460
Gly Val Ala Ala Ile Ser Ala Ala Val Ile Tyr Met Ala Lys Thr Asn
465                               470           475           480
Gly Phe Ile Gly Ile Trp Ile Ala Leu Thr Ile Tyr Met Ala Leu Arg
                               485           490           495
Ala Ile Thr Gly Ile Ala Arg Met Ala Thr Gly Thr Gly Pro Trp Arg
                    500                               505           510
Phe Leu Arg Gly Arg Ser Ser Ser Ser Ser Ser
      515                               520

```

<210> 11
 <211> 16
 <212> PRT
 <213> Arabidopsis thaliana

<400> 11
 Pro Ala Asn Asp Val Thr Leu Pro Ile Lys Glu Asp Asp Ser Ser Asn
 1 5 10 15

<210> 12
 <211> 501
 <212> PRT
 <213> Arabidopsis thaliana

<400> 12
 Met Ser Glu Asp Gly Tyr Asn Thr Asp Phe Pro Arg Asn Pro Leu Tyr
 1 5 10 15
 Ile Phe Phe Ser Asp Phe Arg Ser Val Leu Lys Phe Asp Glu Leu Gly
 20 25 30
 Leu Glu Ile Ala Arg Ile Ala Leu Pro Ala Ala Leu Ala Leu Thr Ala
 35 40 45
 Asp Pro Ile Ala Ser Leu Val Asp Thr Ala Phe Ile Gly Gln Ile Gly
 50 55 60
 Pro Val Glu Leu Ala Ala Val Gly Val Ser Ile Ala Leu Phe Asn Gln
 65 70 75 80
 Val Ser Arg Ile Ala Ile Phe Pro Leu Val Ser Ile Thr Thr Ser Phe
 85 90 95
 Val Ala Glu Glu Asp Ala Cys Ser Ser Gln Gln Asp Thr Val Arg Asp
 100 105 110
 His Lys Glu Cys Ile Glu Ile Gly Ile Asn Asn Pro Thr Glu Glu Thr
 115 120 125
 Ile Glu Leu Ile Pro Glu Lys His Lys Asp Ser Leu Ser Asp Glu Phe
 130 135 140
 Lys Thr Ser Ser Ser Ile Phe Ser Ile Ser Lys Pro Pro Ala Lys Lys
 145 150 155 160
 Arg Asn Ile Pro Ser Ala Ser Ser Ala Leu Ile Ile Gly Gly Val Leu
 165 170 175
 Gly Leu Phe Gln Ala Val Phe Leu Ile Ser Ala Ala Lys Pro Leu Leu
 180 185 190
 Ser Phe Met Gly Val Lys His Asp Ser Pro Met Met Arg Pro Ser Gln
 195 200 205
 Arg Tyr Leu Ser Leu Arg Ser Leu Gly Ala Pro Ala Val Leu Leu Ser
 210 215 220
 Leu Ala Ala Gln Gly Val Phe Arg Gly Phe Lys Asp Thr Thr Thr Pro
 225 230 235 240
 Leu Phe Ala Thr Val Ile Gly Asp Val Thr Asn Ile Ile Leu Asp Pro
 245 250 255

18

Ile Phe Ile Phe Val Phe Arg Leu Gly Val Thr Gly Ala Ala Thr Ala
 260 265 270
 His Val Ile Ser Gln Tyr Leu Met Cys Gly Ile Leu Leu Trp Lys Leu
 275 280 285
 Met Gly Gln Val Asp Ile Phe Asn Met Ser Thr Lys His Leu Gln Phe
 290 295 300
 Cys Arg Phe Met Lys Asn Gly Phe Leu Leu Leu Met Arg Val Ile Ala
 305 310 315 320
 Val Thr Phe Cys Val Thr Leu Ser Ala Ser Leu Ala Ala Arg Glu Gly
 325 330 335
 Ser Thr Ser Met Ala Ala Phe Gln Val Cys Leu Gln Val Trp Leu Ala
 340 345 350
 Thr Ser Leu Leu Ala Asp Gly Tyr Ala Val Ala Gly Gln Ala Ile Leu
 355 360 365
 Ala Ser Ala Phe Ala Lys Lys Asp Tyr Lys Arg Ala Ala Thr Ala
 370 375 380
 Ser Arg Val Leu Gln Leu Gly Leu Val Leu Gly Phe Val Leu Ala Val
 385 390 395 400
 Ile Leu Gly Ala Gly Leu His Phe Gly Ala Arg Val Phe Thr Lys Asp
 405 410 415
 Asp Lys Val Leu His Leu Ile Ser Ile Gly Leu Pro Phe Val Ala Gly
 420 425 430
 Thr Gln Pro Ile Asn Ala Leu Ala Phe Val Phe Asp Gly Val Asn Phe
 435 440 445
 Gly Ala Ser Asp Phe Gly Tyr Ala Ala Ala Ser Leu Val Met Val Ala
 450 455 460
 Ile Val Ser Ile Leu Cys Leu Leu Phe Leu Ser Ser Thr His Gly Phe
 465 470 475 480
 Ile Gly Leu Trp Phe Gly Leu Thr Ile Tyr Met Ser Leu Arg Ala Ala
 485 490 495
 Val Gly Phe Trp Arg
 500

<210> 13

<211> 479

<212> PRT

<213> Arabidopsis thaliana

<400> 13

Met Leu Leu Cys Val Ser Cys Leu Cys Asn Ala Leu Val Ser Val Leu
 1 5 10 15
 Ala Arg Glu Val Asn Gly Val His Thr Gly Val Ala Arg Pro Val Asp
 20 25 30

 Ile Lys Arg Glu Leu Val Met Leu Ser Leu Pro Ala Ile Ala Gly Gln
 35 40 45
 Ala Ile Asp Pro Leu Thr Leu Leu Met Glu Thr Ala Tyr Ile Gly Arg
 50 55 60
 Leu Gly Ser Val Glu Leu Gly Ser Ala Gly Val Ser Met Ala Ile Phe
 65 70 75 80
 Asn Thr Ile Ser Lys Leu Phe Asn Ile Pro Leu Leu Ser Val Ala Thr
 85 90 95
 Ser Phe Val Ala Glu Asp Ile Ala Lys Ile Ala Ala Gln Asp Leu Ala
 100 105 110
 Ser Glu Asp Ser Gln Ser Asp Ile Pro Ser Gln Gly Leu Pro Glu Arg
 115 120 125
 Lys Gln Leu Ser Ser Val Ser Thr Ala Leu Val Leu Ala Ile Gly Ile
 130 135 140

19

Gly Ile Phe Glu Ala Leu Ala Leu Ser Leu Ala Ser Gly Pro Phe Leu
 145 150 155 160
 Arg Leu Met Gly Ile Gln Ser Val Ser Ser Val Gln Arg Met Ser Glu
 165 170 175
 Met Phe Ile Pro Ala Arg Gln Phe Leu Val Leu Arg Ala Leu Gly Ala
 180 185 190
 Pro Ala Tyr Val Val Ser Leu Ala Leu Gln Gly Ile Phe Arg Gly Phe
 195 200 205
 Lys Asp Thr Lys Thr Pro Val Tyr Cys Leu Val Leu Ser Phe Pro Asn
 210 215 220
 Phe His Asn Ser Gly Ile Gly Asn Phe Leu Ala Val Phe Leu Phe Pro
 225 230 235 240
 Leu Phe Ile Tyr Lys Phe Arg Met Gly Val Ala Gly Ala Ala Ile Ser
 245 250 255
 Ser Val Ile Ser Gln Met Val Leu Asn Pro Phe Pro Leu Ile His Arg
 260 265 270
 Tyr Thr Val Ala Ile Leu Met Leu Ile Leu Leu Asn Lys Arg Val Ile
 275 280 285
 Leu Leu Pro Pro Lys Ile Gly Ser Leu Lys Phe Gly Asp Tyr Leu Lys
 290 295 300
 Ser Gly Gly Phe Val Leu Gly Arg Thr Leu Ser Val Leu Val Thr Met
 305 310 315 320
 Thr Val Ala Thr Ser Met Ala Ala Arg Gln Gly Val Phe Ala Met Ala
 325 330 335
 Ala His Gln Ile Cys Met Gln Val Trp Leu Ala Val Ser Leu Leu Thr
 340 345 350
 Asp Ala Leu Ala Ser Ser Gly Gln Ala Leu Ile Ala Ser Ser Ala Ser
 355 360 365
 Lys Arg Asp Phe Glu Gly Val Lys Glu Phe Ile Phe Thr Phe Trp Gly
 370 375 380
 Cys Tyr Leu Ile Ser Cys Tyr Ile Tyr Ile Tyr Arg Glu Arg Cys Asn
 385 390 395 400
 Val Phe Gly Val Val Gln Ile Gly Val Val Thr Gly Ile Ala Leu Ala
 405 410 415
 Ile Val Leu Gly Met Ser Phe Ser Ser Ile Ala Asp Gly Gly Gly Arg
 420 425 430
 Asn Ile Ile Ser Val His Ala Val Cys Thr Gly Arg Val Gly Ala Lys
 435 440 445
 Trp Ser Val Gly Gly Ala Glu His Val His Gly Ile Ala Asp Gly Gly
 450 455 460
 Trp Ile Gln Gln Val Lys Lys Glu Leu Pro Val Ser Ile Tyr Lys
 465 470 475

<210> 14

<211> 484

<212> PRT

<213> Arabidopsis thaliana

<400> 14

Met Ala Asp Pro Ala Thr Ser Ser Pro Leu Leu Asp Asp His Val Gly
 1 5 10 15
 Gly Glu Asp Glu Arg Gly Arg Arg Ser Arg Ser Ser Thr Leu Val Gln
 20 25 30
 Lys Val Ile Asp Val Glu Glu Ala Lys Ala Gln Met Ile Tyr Ser Leu
 35 40 45
 Pro Met Ile Leu Thr Asn Val Phe Tyr Tyr Cys Ile Pro Ile Thr Ser
 50 55 60

Val	Met	Phe	Ala	Ser	His	Leu	Gly	Gln	Leu	Glu	Leu	Ala	Gly	Ala	Thr	65	70	75	80
Leu	Ala	Asn	Ser	Trp	Ala	Thr	Val	Ser	Gly	Phe	Ala	Phe	Met	Val	Gly	85	90		95
Leu	Ser	Gly	Ser	Leu	Glu	Thr	Leu	Cys	Gly	Gln	Gly	Phe	Gly	Ala	Lys	100	105		110
Arg	Tyr	Arg	Met	Leu	Gly	Val	His	Leu	Gln	Ser	Ser	Cys	Ile	Val	Ser	115	120		125
Leu	Val	Phe	Ser	Ile	Leu	Ile	Thr	Ile	Phe	Trp	Phe	Phe	Thr	Glu	Ser	130	135		140
Ile	Phe	Gly	Leu	Leu	Arg	Gln	Asp	Pro	Ser	Ile	Ser	Lys	Gln	Ala	Ala	145	150	155	160
Leu	Tyr	Met	Lys	Tyr	Gln	Ala	Pro	Gly	Leu	Leu	Ala	Tyr	Gly	Phe	Leu	165	170		175
Gln	Asn	Ile	Leu	Arg	Phe	Cys	Gln	Thr	Gln	Ser	Ile	Ile	Ala	Pro	Leu	180	185		190
Val	Ile	Phe	Ser	Phe	Val	Pro	Leu	Val	Ile	Asn	Ile	Ala	Thr	Ala	Tyr	195	200		205
Val	Leu	Val	Tyr	Val	Ala	Gly	Leu	Gly	Phe	Ile	Gly	Ala	Pro	Ile	Ala	210	215		220
Thr	Ser	Ile	Ser	Leu	Trp	Ile	Ala	Phe	Leu	Ser	Leu	Gly	Thr	Tyr	Val	225	230	235	240
Met	Cys	Ser	Glu	Lys	Phe	Lys	Glu	Thr	Trp	Thr	Gly	Phe	Ser	Leu	Glu	245	250		255
Ser	Phe	Arg	Tyr	Ile	Val	Ile	Asn	Leu	Thr	Leu	Ser	Leu	Pro	Ser	Ala	260	265		270
Ala	Met	Leu	Lys	Arg	Leu	Tyr	Cys	Cys	Asn	Ser	Leu	Glu	Tyr	Trp	Ala	275	280		285
Phe	Glu	Ile	Leu	Val	Phe	Leu	Ala	Gly	Val	Met	Pro	Asn	Pro	Glu	Ile	290	295	300	
Asn	Thr	Ser	Leu	Val	Ala	Ile	Cys	Val	Asn	Thr	Glu	Ala	Ile	Ser	Tyr	305	310	315	320
Met	Leu	Thr	Tyr	Gly	Leu	Ser	Ala	Ala	Ala	Ser	Thr	Arg	Val	Ser	Asn	325	330		335
Glu	Leu	Gly	Ala	Gly	Asn	Val	Lys	Gly	Ala	Lys	Lys	Ala	Thr	Ser	Val	340	345		350
Ser	Val	Lys	Leu	Ser	Leu	Val	Leu	Ala	Leu	Gly	Val	Val	Ile	Val	Leu	355	360	365	
Leu	Val	Gly	His	Asp	Gly	Trp	Val	Gly	Leu	Phe	Ser	Asp	Ser	Tyr	Val	370	375	380	
Ile	Lys	Glu	Glu	Phe	Ala	Ser	Leu	Arg	Phe	Phe	Leu	Ala	Ala	Ser	Ile	385	390	395	400
Thr	Leu	Asp	Ser	Ile	Gln	Gly	Val	Leu	Ser	Gly	Val	Ala	Arg	Gly	Cys	405	410		415
Gly	Trp	Gln	Arg	Leu	Val	Thr	Val	Ile	Asn	Leu	Ala	Thr	Phe	Tyr	Leu	420	425		430
Ile	Gly	Met	Pro	Ile	Ala	Ala	Phe	Cys	Gly	Phe	Lys	Leu	Lys	Phe	Tyr	435	440	445	
Ala	Lys	Gly	Leu	Trp	Ile	Gly	Leu	Ile	Cys	Gly	Ile	Phe	Cys	Gln	Ser	450	455	460	
Ser	Ser	Leu	Leu	Leu	Met	Thr	Ile	Phe	Arg	Lys	Trp	Thr	Lys	Leu	Asn	465	470	475	480
Val	Ala	Thr	Val																

<210> 15
 <211> 507
 <212> PRT
 <213> Arabidopsis thaliana

<400> 15

Met	Ser	Ser	Thr	Glu	Thr	Tyr	Glu	Pro	Leu	Leu	Thr	Arg	Leu	His	Ser
1				5					10					15	
Asp	Ser	Gln	Ile	Thr	Glu	Arg	Ser	Ser	Pro	Glu	Ile	Glu	Glu	Phe	Leu
			20					25					30		
Arg	Arg	Arg	Gly	Ser	Thr	Val	Thr	Pro	Arg	Trp	Trp	Leu	Lys	Leu	Ala
		35					40					45			
Val	Trp	Glu	Ser	Lys	Leu	Leu	Trp	Thr	Leu	Ser	Gly	Ala	Ser	Ile	Val
	50					55					60				
Val	Ser	Val	Leu	Asn	Tyr	Met	Leu	Ser	Phe	Val	Thr	Val	Met	Phe	Thr
65					70					75					80
Gly	His	Leu	Gly	Ser	Leu	Gln	Leu	Ala	Gly	Ala	Ser	Ile	Ala	Thr	Val
				85					90					95	
Gly	Ile	Gln	Gly	Leu	Ala	Tyr	Gly	Ile	Met	Leu	Gly	Met	Ala	Ser	Ala
			100					105					110		
Val	Gln	Thr	Val	Cys	Gly	Gln	Ala	Tyr	Gly	Ala	Arg	Gln	Tyr	Ser	Ser
		115					120					125			
Met	Gly	Ile	Ile	Cys	Gln	Arg	Ala	Met	Val	Leu	His	Leu	Ala	Ala	Ala
	130					135					140				
Val	Phe	Leu	Thr	Phe	Leu	Tyr	Trp	Tyr	Ser	Gly	Pro	Ile	Leu	Lys	Thr
145					150					155					160
Met	Gly	Gln	Ser	Val	Ala	Ile	Ala	His	Glu	Gly	Gln	Ile	Phe	Ala	Arg
				165					170					175	
Gly	Met	Ile	Pro	Gln	Ile	Tyr	Ala	Phe	Ala	Leu	Ala	Cys	Pro	Met	Gln
			180					185					190		
Arg	Phe	Leu	Gln	Ala	Gln	Asn	Ile	Val	Asn	Pro	Leu	Ala	Tyr	Met	Ser
		195				200						205			
Leu	Gly	Val	Phe	Leu	Leu	His	Thr	Leu	Leu	Thr	Trp	Leu	Val	Thr	Asn
	210					215					220				
Val	Leu	Asp	Phe	Gly	Leu	Leu	Gly	Ala	Ala	Leu	Ile	Leu	Ser	Phe	Ser
225					230					235					240
Trp	Trp	Leu	Leu	Val	Ala	Val	Asn	Gly	Met	Tyr	Ile	Leu	Met	Ser	Pro
				245					250					255	
Asn	Cys	Lys	Glu	Thr	Trp	Thr	Gly	Phe	Ser	Thr	Arg	Ala	Phe	Arg	Gly
			260					265					270		
Ile	Trp	Pro	Tyr	Phe	Lys	Leu	Thr	Val	Ala	Ser	Ala	Val	Met	Leu	Cys
		275					280					285			
Leu	Glu	Ile	Trp	Tyr	Asn	Gln	Gly	Leu	Val	Ile	Ile	Ser	Gly	Leu	Leu
	290					295						300			
Ser	Asn	Pro	Thr	Ile	Ser	Leu	Asp	Ala	Ile	Ser	Ile	Cys	Met	Tyr	Tyr
305					310					315					320
Leu	Asn	Trp	Asp	Met	Gln	Phe	Met	Leu	Gly	Leu	Ser	Ala	Ala	Ile	Ser
				325					330					335	
Val	Arg	Val	Ser	Asn	Glu	Leu	Gly	Ala	Gly	Asn	Pro	Arg	Val	Ala	Met
			340					345					350		
Leu	Ser	Val	Val	Val	Val	Asn	Ile	Thr	Thr	Val	Leu	Ile	Ser	Ser	Val
		355					360					365			
Leu	Cys	Val	Ile	Val	Leu	Val	Phe	Arg	Val	Gly	Leu	Ser	Lys	Ala	Phe
	370					375					380				
Thr	Ser	Asp	Ala	Glu	Val	Ile	Ala	Ala	Val	Ser	Asp	Leu	Phe	Pro	Leu
385					390					395					400
Leu	Ala	Val	Ser	Ile	Phe	Leu	Asn	Gly	Ile	Gln	Pro	Ile	Leu	Ser	Gly
				405					410					415	

Val Ala Ile Gly Ser Gly Trp Gln Ala Val Val Ala Tyr Val Asn Leu
 420 425 430
 Val Thr Tyr Tyr Val Ile Gly Leu Pro Ile Gly Cys Val Leu Gly Phe
 435 440 445
 Lys Thr Ser Leu Gly Val Ala Gly Ile Trp Trp Gly Met Ile Ala Gly
 450 455 460
 Val Ile Leu Gln Thr Leu Thr Leu Ile Val Leu Thr Leu Lys Thr Asn
 465 470 475 480
 Trp Thr Ser Glu Val Glu Asn Ala Ala Gln Arg Val Lys Thr Ser Ala
 485 490 495
 Thr Glu Asn Gln Glu Met Ala Asn Ala Gly Val
 500 505

<210> 16
 <211> 536
 <212> PRT
 <213> Arabidopsis thaliana

<400> 16
 Thr Leu Gln Gln Glu Ala Trp Gln Gln Gly Tyr Asp Ser His Asp Arg
 1 5 10 15
 Lys Arg Leu Leu Asp Glu Glu Arg Asp Leu Leu Ile Asp Asn Lys Leu
 20 25 30
 Leu Ser Gln His Gly Asn Gly Gly Gly Asp Ile Glu Ser His Gly His
 35 40 45
 Gly Gln Ala Ile Gly Pro Asp Glu Glu Glu Arg Pro Ala Glu Ile Ala
 50 55 60
 Asn Thr Trp Glu Ser Ala Ile Glu Ser Gly Gln Lys Ile Ser Thr Thr
 65 70 75 80
 Phe Lys Arg Glu Thr Gln Val Ile Thr Met Asn Ala Leu Pro Leu Ile
 85 90 95
 Phe Thr Phe Ile Leu Gln Asn Ser Leu Ser Leu Ala Ser Ile Phe Ser
 100 105 110
 Val Ser His Leu Gly Thr Lys Glu Leu Gly Gly Val Thr Leu Gly Ser
 115 120 125
 Met Thr Ala Asn Ile Thr Gly Leu Ala Ala Ile Gln Gly Leu Cys Thr
 130 135 140
 Cys Leu Asp Thr Leu Cys Ala Gln Ala Tyr Gly Ala Lys Asn Tyr His
 145 150 155 160
 Leu Val Gly Val Leu Val Gln Arg Cys Ala Val Ile Thr Ile Leu Ala
 165 170 175
 Phe Leu Pro Met Met Tyr Val Trp Phe Val Trp Ser Glu Lys Ile Leu
 180 185 190
 Ala Leu Met Ile Pro Glu Arg Glu Leu Cys Ala Leu Ala Asn Tyr
 195 200 205
 Leu Arg Val Thr Ala Phe Gly Val Pro Gly Phe Ile Leu Phe Glu Cys
 210 215 220
 Gly Lys Arg Phe Leu Gln Cys Gln Gly Ile Phe His Ala Ser Thr Ile
 225 230 235 240
 Val Leu Phe Val Cys Ala Pro Leu Asn Ala Leu Met Asn Tyr Leu Leu
 245 250 255
 Val Trp Asn Asp Lys Ile Gly Ile Gly Tyr Leu Gly Ala Pro Leu Ser
 260 265 270
 Val Val Ile Asn Tyr Trp Leu Met Thr Leu Gly Leu Leu Ile Tyr Ala
 275 280 285
 Met Thr Thr Lys His Lys Glu Arg Pro Leu Lys Cys Trp Asn Gly Ile
 290 295 300

Ile Pro Lys Glu Gln Ala Phe Lys Asn Trp Arg Lys Met Ile Asn Leu
 305 310 315 320
 Ala Ile Pro Gly Val Val Met Val Glu Ala Glu Phe Leu Gly Phe Glu
 325 330 335
 Val Leu Thr Ile Phe Ala Ser His Leu Gly Thr Asp Ala Leu Gly Ala
 340 345 350
 Gln Ser Ile Val Ala Thr Ile Ala Ser Leu Ala Tyr Gln Val Pro Phe
 355 360 365
 Ser Ile Ser Val Ser Thr Ser Thr Arg Val Ala Asn Phe Ile Gly Ala
 370 375 380
 Ser Leu Tyr Asp Ser Cys Met Ile Thr Cys Arg Val Ser Leu Leu Leu
 385 390 395 400
 Ser Phe Val Cys Ser Ser Met Asn Met Phe Val Ile Cys Arg Tyr Lys
 405 410 415
 Glu Gln Ile Ala Ser Leu Phe Ser Thr Glu Ser Ala Val Val Lys Met
 420 425 430
 Val Val Asp Thr Leu Pro Leu Leu Ala Phe Met Gln Leu Phe Asp Ala
 435 440 445
 Phe Asn Ala Ser Thr Ala Gly Cys Leu Arg Gly Gln Gly Arg Gln Lys
 450 455 460
 Ile Gly Gly Tyr Ile Asn Leu Val Ala Phe Tyr Cys Leu Cys Val Pro
 465 470 475 480
 Met Ala Tyr Val Leu Ala Phe Leu Tyr His Ile Gly Val Gly Leu Trp
 485 490 495
 Leu Gly Thr Thr Ser Ala Leu Val Met Met Ser Val Cys Gln Gly Tyr
 500 505 510
 Ala Val Pro His Gln Asp Arg Arg Arg Ile Leu Gly Ala Ala Arg Lys
 515 520 525
 Arg Asn Ala Glu Thr His Thr Ser
 530 535

<210> 17

<211> 456

<212> PRT

<213> Arabidopsis thaliana

<400> 17

Met His Arg Tyr Lys Glu Glu Ala Ser Ser Leu Ile Lys Leu Ala Thr
 1 5 10 15
 Pro Val Leu Ile Ala Ser Val Ala Gln Thr Gly Met Gly Phe Val Asp
 20 25 30
 Thr Val Met Ala Gly Gly Val Thr Gln Thr Asp Met Ala Ala Val Ser
 35 40 45
 Val Ala Ser Ser Ile Trp Leu Pro Ser Ile Leu Phe Gly Ile Gly Leu
 50 55 60
 Leu Met Ala Leu Val Pro Val Val Ala Gln Leu Asn Gly Ser Ala Arg
 65 70 75 80
 Arg Glu Lys Ile Pro Phe Glu Ile Gln Gln Gly Val Val Leu Ala Leu
 85 90 95
 Leu Ile Ser Ile Pro Ile Ile Gly Val Leu Leu Gln Thr Gln Phe Ile
 100 105 110
 Leu Gln Leu Met Asp Val Glu Ala Val Met Ala Asp Lys Thr Val Gly
 115 120 125
 Tyr Ile His Ala Val Ile Phe Ala Val Pro Ala Phe Leu Leu Phe Gln
 130 135 140
 Thr Leu Arg Ser Phe Thr Asp Gly Met Ser Leu Thr Lys Pro Ala Met
 145 150 155 160

25

Phe Val Ser Val Leu Ile Met Leu Val Leu Trp Asn Ala Gly Tyr Ile
 100 105 110
 Ile Arg Ser Met Glu Asn Ile Asp Pro Ala Leu Ala Asp Lys Ala Val
 115 120 125
 Gly Tyr Leu Arg Ala Leu Leu Trp Gly Ala Pro Gly Tyr Leu Phe Phe
 130 135 140
 Gln Val Ala Arg Asn Gln Cys Glu Gly Leu Ala Lys Thr Lys Pro Gly
 145 150 155 160
 Met Val Met Gly Phe Ile Gly Leu Leu Val Asn Ile Pro Val Asn Tyr
 165 170 175
 Ile Phe Ile Tyr Gly His Phe Gly Met Pro Glu Leu Gly Gly Val Gly
 180 185 190
 Cys Gly Val Ala Thr Ala Ala Val Tyr Trp Val Met Phe Leu Ala Met
 195 200 205

 Val Ser Tyr Ile Lys Arg Ala Arg Ser Met Arg Asp Ile Arg Asn Glu
 210 215 220
 Lys Gly Thr Ala Lys Pro Asp Pro Ala Val Met Lys Arg Leu Ile Gln
 225 230 235 240
 Leu Gly Leu Pro Ile Ala Leu Ala Leu Phe Phe Glu Val Thr Leu Phe
 245 250 255
 Ala Val Val Ala Leu Leu Val Ser Pro Leu Gly Ile Val Asp Val Ala
 260 265 270
 Gly His Gln Ile Ala Leu Asn Phe Ser Ser Leu Met Phe Val Leu Pro
 275 280 285
 Met Ser Leu Ala Ala Ala Val Thr Ile Arg Val Gly Tyr Arg Leu Gly
 290 295 300
 Gln Gly Ser Thr Leu Asp Ala Gln Thr Ala Ala Arg Thr Gly Leu Met
 305 310 315 320
 Val Gly Val Cys Met Ala Thr Leu Thr Ala Ile Phe Thr Val Ser Leu
 325 330 335
 Arg Glu Gln Ile Ala Leu Leu Tyr Asn Asp Asn Pro Glu Val Val Thr
 340 345 350
 Leu Ala Ala His Leu Met Leu Leu Ala Ala Val Tyr Gln Ile Ser Asp
 355 360 365
 Ser Ile Gln Val Ile Gly Ser Gly Ile Leu Arg Gly Tyr Lys Asp Thr
 370 375 380
 Arg Ser Ile Phe Tyr Ile Thr Phe Thr Ala Tyr Trp Val Leu Gly Leu
 385 390 395 400
 Pro Ser Gly Tyr Ile Leu Ala Leu Thr Asp Leu Val Val Glu Pro Met
 405 410 415
 Gly Pro Ala Gly Phe Trp Ile Gly Phe Ile Ile Gly Leu Thr Ser Ala
 420 425 430
 Ala Ile Met Met Met Leu Arg Met Arg Phe Leu Gln Arg Leu Pro Ser
 435 440 445
 Ala Ile Ile Leu Gln Arg Ala Ser Arg
 450 455

<210> 19

<211> 459

<212> PRT

<213> Arabidopsis thaliana

<400> 19

Met Pro Pro Gly Val Ala Val Cys Phe Ser Ser Leu Phe Ile Arg Leu
 1 5 10 15
 Val Cys Met Ala Phe Leu Thr Ser Ser Asp Lys Ala Leu Trp His Leu
 20 25 30

Ala Leu Pro Met Ile Phe Ser Asn Ile Thr Val Pro Leu Leu Gly Leu
 35 40 45
 Val Asp Thr Ala Val Ile Gly His Leu Asp Ser Pro Val Tyr Leu Gly
 50 55 60
 Gly Val Ala Val Gly Ala Thr Ser Phe Leu Phe Met Leu Leu
 65 70 75 80
 Leu Phe Leu Arg Met Ser Thr Thr Gly Leu Thr Ala Gln Ala Tyr Gly
 85 90 95
 Ala Lys Asn Pro Gln Ala Leu Ala Arg Thr Leu Val Gln Pro Leu Leu
 100 105 110
 Leu Ala Leu Gly Ala Gly Ala Leu Ile Ala Leu Leu Arg Thr Pro Ile
 115 120 125
 Ile Asp Leu Ala Leu His Ile Val Gly Gly Ser Glu Ala Val Leu Glu
 130 135 140

 Gln Ala Arg Arg Phe Leu Glu Ile Arg Trp Leu Ser Ala Pro Ala Ser
 145 150 155 160
 Leu Ala Asn Leu Val Leu Leu Gly Trp Leu Leu Gly Val Gln Tyr Ala
 165 170 175
 Arg Ala Pro Val Ile Leu Leu Val Val Gly Asn Ile Leu Asn Ile Val
 180 185 190
 Leu Asp Val Trp Leu Val Met Gly Leu His Met Asn Val Gln Gly Ala
 195 200 205
 Ala Leu Ala Thr Val Ile Ala Glu Tyr Ala Thr Leu Leu Ile Gly Leu
 210 215 220
 Leu Met Val Arg Lys Ile Leu Lys Leu Arg Gly Ile Ser Gly Glu Met
 225 230 235 240
 Leu Lys Thr Ala Trp Arg Gly Asn Phe Arg Arg Leu Leu Ala Leu Asn
 245 250 255
 Arg Asp Ile Met Leu Arg Ser Leu Leu Leu Gln Leu Cys Phe Gly Ala
 260 265 270
 Ile Thr Val Leu Gly Ala Arg Leu Gly Ser Asp Ile Ile Ala Val Asn
 275 280 285
 Ala Val Leu Met Thr Leu Leu Thr Phe Thr Ala Tyr Ala Leu Asp Gly
 290 295 300
 Phe Ala Tyr Ala Val Glu Ala His Ser Gly Gln Ala Tyr Gly Ala Arg
 305 310 315 320
 Asp Gly Ser Gln Leu Leu Asp Val Trp Arg Ala Ala Cys Arg Gln Ser
 325 330 335
 Gly Ile Val Ala Leu Leu Phe Ser Val Val Tyr Leu Leu Ala Gly Glu
 340 345 350
 His Ile Ile Ala Leu Leu Thr Ser Leu Thr Gln Ile Gln Gln Leu Ala
 355 360 365
 Asp Arg Tyr Leu Ile Trp Gln Val Ile Leu Pro Val Val Gly Val Trp
 370 375 380
 Cys Tyr Leu Leu Asp Gly Met Phe Ile Gly Ala Thr Arg Ala Thr Glu
 385 390 395 400
 Met Arg Asn Ser Met Ala Val Ala Ala Gly Phe Ala Leu Thr Leu
 405 410 415
 Leu Thr Leu Pro Trp Leu Gly Asn His Ala Leu Trp Leu Ala Leu Thr
 420 425 430
 Val Phe Leu Ala Leu Arg Gly Leu Ser Leu Ala Ala Ile Trp Arg Arg
 435 440 445
 His Trp Arg Asn Gly Thr Trp Phe Ala Ala Thr
 450 455

<210> 20

<211> 1868

<212> DNA

<213> *Arabidopsis thaliana*

<220>

<221> CDS

<222> (118)...(1695)

<400> 20

```

aaataatccc ctctaaactc tcctagatac tcactcatca ctactcatct caagttcacg 60
tgactactta tataagcggt gactacataa agagacagtt acagaggaaa aagatct atg 120
                                         Met
                                         1

```

```

acg gaa act ggt gat gat ctt gct acg gtg aag aag cca atc cca ttt 168
Thr Glu Thr Gly Asp Asp Leu Ala Thr Val Lys Lys Pro Ile Pro Phe
                    5                      10                      15

ctc gtt atc ttc aaa gat tta aga cat gta ttc agt agg gac aca act 216
Leu Val Ile Phe Lys Asp Leu Arg His Val Phe Ser Arg Asp Thr Thr
                    20                      25                      30

ggg cga gag att cta ggc atc gcg ttt cca gca gct ttg gct tta gct 264
Gly Arg Glu Ile Leu Gly Ile Ala Phe Pro Ala Ala Leu Ala Leu Ala
                    35                      40                      45

gct gat cca atc gct tct ctg att gat acc gct ttt gtc ggg cgt tta 312
Ala Asp Pro Ile Ala Ser Leu Ile Asp Thr Ala Phe Val Gly Arg Leu
                    50                      55                      60                      65

gga gcg gtt cag cta gcg gcg gtt gga gtt tcc att gcc ata ttc aat 360
Gly Ala Val Gln Leu Ala Ala Val Gly Val Ser Ile Ala Ile Phe Asn
                    70                      75                      80

caa gct tct aga att acg ata ttc cca ctt gtg agc ctc aca act tca 408
Gln Ala Ser Arg Ile Thr Ile Phe Pro Leu Val Ser Leu Thr Thr Ser
                    85                      90                      95

ttt gtg gca gag gaa gac acg atg gag aag atg aaa gaa gaa gca aac 456
Phe Val Ala Glu Glu Asp Thr Met Glu Lys Met Lys Glu Glu Ala Asn
                    100                      105                      110

aaa gcc aat ctt gtt cat gca gaa act ata ctt gtt caa gat tct ttg 504
Lys Ala Asn Leu Val His Ala Glu Thr Ile Leu Val Gln Asp Ser Leu
                    115                      120                      125

gaa aag ggc att tct tca cct aca agt aac gat acc aac cag cca cag 552
Glu Lys Gly Ile Ser Ser Pro Thr Ser Asn Asp Thr Asn Gln Pro Gln
                    130                      135                      140                      145

caa cct cca gct ccg gat aca aag tca aat agc gga aac aaa tcg aat 600
Gln Pro Pro Ala Pro Asp Thr Lys Ser Asn Ser Gly Asn Lys Ser Asn
                    150                      155                      160

aaa aag gag aag agg acc att aga aca gca tca aca gct atg atc ttg 648
Lys Lys Glu Lys Arg Thr Ile Arg Thr Ala Ser Thr Ala Met Ile Leu
                    165                      170                      175

```

ggg tta atc ctt ggc ctt gtg caa gct att ttc ttg att ttc agt tca	696
Gly Leu Ile Leu Gly Leu Val Gln Ala Ile Phe Leu Ile Phe Ser Ser	
180 185 190	
aag ttg ctt cta ggc gtc atg gga gtg aaa cca aat tca cca atg tta	744
Lys Leu Leu Leu Gly Val Met Gly Val Lys Pro Asn Ser Pro Met Leu	
195 200 205	
tca cca gca cac aag tac ttg agc ata cga gct ttg ggg gct cct gca	792
Ser Pro Ala His Lys Tyr Leu Ser Ile Arg Ala Leu Gly Ala Pro Ala	
210 215 220 225	
ttg ctt cta tct ctt gct atg caa ggc atc ttt cgt gga ttc aag gac	840
Leu Leu Leu Ser Leu Ala Met Gln Gly Ile Phe Arg Gly Phe Lys Asp	
230 235 240	
acc aaa act cct ctc ttt gcc act gtc gta gca gat gtt atc aac ata	888
Thr Lys Thr Pro Leu Phe Ala Thr Val Val Ala Asp Val Ile Asn Ile	
245 250 255	
gtt ctc gac ccc atc ttc att ttt gtg ctt cgt cta ggg atc atc ggt	936
Val Leu Asp Pro Ile Phe Ile Phe Val Leu Arg Leu Gly Ile Ile Gly	
260 265 270	
gca gcc att gcc cat gtc att tct cag tac ttc atg act cta ata ttg	984
Ala Ala Ile Ala His Val Ile Ser Gln Tyr Phe Met Thr Leu Ile Leu	
275 280 285	
ttc gtc ttc ctc gca aag aaa gtt aat ttg att cca cca aac ttc ggg	1032
Phe Val Phe Leu Ala Lys Lys Val Asn Leu Ile Pro Pro Asn Phe Gly	
290 295 300 305	
gat ttg cag ttt gga agg ttc ctt aaa aat ggg cta cta ttg ctg gcg	1080
Asp Leu Gln Phe Gly Arg Phe Leu Lys Asn Gly Leu Leu Leu Leu Ala	
310 315 320	
agg acc ata gca gtg acg ttt tgt cag acc tta gca gca gca atg gcg	1128
Arg Thr Ile Ala Val Thr Phe Cys Gln Thr Leu Ala Ala Ala Met Ala	
325 330 335	
gcg cgg ctg ggt aca aca cca atg gct gct ttt cag att tgt tta caa	1176
Ala Arg Leu Gly Thr Thr Pro Met Ala Ala Phe Gln Ile Cys Leu Gln	
340 345 350	
gta tgg tta act tct tct ctt ctc aat gat ggt ctt gcc gtt gct ggt	1224
Val Trp Leu Thr Ser Ser Leu Leu Asn Asp Gly Leu Ala Val Ala Gly	
355 360 365	
cag gcg att ctg gct tgt tcg ttt gct gag aag gac tat aac aaa gtg	1272
Gln Ala Ile Leu Ala Cys Ser Phe Ala Glu Lys Asp Tyr Asn Lys Val	
370 375 380 385	
act gct gtt gca tcc cgt gtt cta cag atg ggt ttt gtg tta gga ctt	1320
Thr Ala Val Ala Ser Arg Val Leu Gln Met Gly Phe Val Leu Gly Leu	
390 395 400	
gga ctg tcc gtt ttt gtt gga cta ggt ctc tac ttt ggt gcc gga gtt	1368
Gly Leu Ser Val Phe Val Gly Leu Gly Leu Tyr Phe Gly Ala Gly Val	
405 410 415	

ttc tcc aag gac cct gct gtt att cac ctc atg gcc atc gga ata ccg	1416
Phe Ser Lys Asp Pro Ala Val Ile His Leu Met Ala Ile Gly Ile Pro	
420 425 430	
ttt ata gca gca acg cag cca ata aac tct ctc gcc ttt gta ttg gat	1464
Phe Ile Ala Ala Thr Gln Pro Ile Asn Ser Leu Ala Phe Val Leu Asp	
435 440 445	
gga gtc aat ttt gga gca tct gat ttt gct tac act gca tac tcc atg	1512
Gly Val Asn Phe Gly Ala Ser Asp Phe Ala Tyr Thr Ala Tyr Ser Met	
450 455 460 465	
gtg gga gtg gcg gcc ata agc att gca gca gta ata tat atg gca aag	1560
Val Gly Val Ala Ala Ile Ser Ile Ala Ala Val Ile Tyr Met Ala Lys	
470 475 480	
acc aat ggt ttc ata gga ata tgg ata gct ctt aca atc tat atg gct	1608
Thr Asn Gly Phe Ile Gly Ile Trp Ile Ala Leu Thr Ile Tyr Met Ala	
485 490 495	
ctc cgg gct att act gga att gcc agg atg gcg aca gga act gga ccg	1656
Leu Arg Ala Ile Thr Gly Ile Ala Arg Met Ala Thr Gly Thr Gly Pro	
500 505 510	
tgg agg ttc ttg cgt gga cga tca tcc tct tca tct tcc taggaacttag	1705
Trp Arg Phe Leu Arg Gly Arg Ser Ser Ser Ser Ser Ser	
515 520 525	
tttatttata acgagttgca tctcttcttc cttcttcggt tttgtttatg gttctttgtgt	1765
ttgtttttca acatctttgtt cgagagaccg ttatcatatt atcagtttca cataaataat	1825
gcatattttt aagtcattaa aataaaaaaaaa aaaaaaaaaa aaa	1868